

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 26, 2005, 17:39:01 / Search time 8 Seconds  
(without alignments)  
131.089 Million cell updates/sec

Title: US-10-041-859a-2

Perfect score: 1887  
Sequence: 1 MELTKVAKNGAATLVMLKN.....TDKCPKCRRTFTNAVLYPS 346

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 17545 seqs, 3030971 residues

Total number of hits satisfying chosen parameters: 17545

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : Published Applications AA.New:\*  
1: /cgn2\_6/pcodata/2/pubppaa/US10\_NEW\_PUB.pap:\*  
2: /cgn2\_6/pcodata/2/pubppaa/US06\_NEW\_PUB.pap:\*  
3: /cgn2\_6/pcodata/2/pubppaa/US07\_NEW\_PUB.pap:\*  
4: /cgn2\_6/pcodata/2/pubppaa/US08\_NEW\_PUB.pap:\*  
5: /cgn2\_6/pcodata/2/pubppaa/US09\_NEW\_PUB.pap:\*  
6: /cgn2\_6/pcodata/2/pubppaa/PCT\_NEW\_PUB.pap:\*  
7: /cgn2\_6/pcodata/2/pubppaa/US11\_NEW\_PUB.pap:\*  
8: /cgn2\_6/pcodata/2/pubppaa/US60\_NEW\_PUB.pap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	326	17.3	355	US-11-135-855-44	Sequence 44, Appl
2	225	11.9	255	US-11-135-855-45	Sequence 45, Appl
3	98.5	5.2	574	US-10-821-234-1624	Sequence 1624, Ap
4	88.5	4.7	1560	US-11-059-982-1	Sequence 1, Appl
5	82.5	4.4	1493	US-11-004-057-21	Sequence 21, Appl
6	79.5	4.2	543	US-10-689-742-78	Sequence 78, Appl
7	78.5	4.2	1493	US-11-004-057-4	Sequence 4, Appl
8	77	4.1	2897	US-10-499-715-2	Sequence 2, Appl
9	75.5	4.0	328	US-10-821-234-1671	Sequence 1671, Ap
10	74.5	3.9	428	US-11-074-176-364	Sequence 364, App
11	74	3.9	345	US-10-821-234-1104	Sequence 1104, Ap
12	73.5	3.9	525	US-10-131-826A-56	Sequence 56, Appl
13	73.5	3.9	708	US-10-821-234-917	Sequence 917, Appl
14	71.5	3.8	1048	US-10-392-234A-20	Sequence 20, Appl
15	71	3.8	379	US-10-131-826A-216	Sequence 216, Appl
16	71	3.8	758	US-10-467-962B-12	Sequence 12, Appl
17	70.5	3.7	445	US-10-793-626-2858	Sequence 2858, Ap
18	70	3.7	552	US-10-821-234-1022	Sequence 1022, Ap
19	69.5	3.7	1299	US-10-821-234-1145	Sequence 1145, Ap
20	69	3.7	745	US-10-858-730-224	Sequence 224, App
21	69	3.7	1302	US-11-004-057-6	Sequence 6, Appl
22	68.5	3.6	1048	US-10-392-234A-14	Sequence 14, Appl
23	68	3.6	331	US-10-821-234-1650	Sequence 1650, Ap
24	67.5	3.6	242	US-10-821-234-1078	Sequence 1078, Ap
25	67.5	3.6	836	US-10-821-234-1559	Sequence 1559, Ap

26	67	3.6	153	1	US-10-821-234-1355	Sequence 1355, Ap
27	67	3.6	1107	7	US-11-057-058-41	Sequence 41, Appl
28	67	3.6	1476	7	US-10-647-956A-4	Sequence 4, Appl
29	66.5	3.5	325	1	US-10-131-826A-516	Sequence 516, App
30	66.5	3.5	396	7	US-11-109-156-10	Sequence 10, Appl
31	66	3.5	365	1	US-10-821-234-1575	Sequence 1575, Ap
32	66	3.5	488	1	US-10-984-376-1	Sequence 1, Appl
33	66	3.5	488	1	US-10-984-376-4	Sequence 4, Appl
34	65.5	3.5	211	7	US-11-132-839-12	Sequence 12, Appl
35	65.5	3.5	1049	1	US-10-392-234A-12	Sequence 12, Appl
36	65	3.4	745	1	US-10-131-826A-68	Sequence 68, Appl
37	65	3.4	745	7	US-11-135-855-37	Sequence 37, Appl
38	65	3.4	1970	1	US-10-821-234-1641	Sequence 1641, Ap
39	64	3.4	457	1	US-10-982-545-8	Sequence 8, Appl
40	64	3.4	457	1	US-10-982-545-13	Sequence 13, Appl
41	64	3.4	651	1	US-10-994-820A-34	Sequence 34, Appl
42	64	3.4	1467	1	US-10-821-234-1096	Sequence 1096, Ap
43	63.5	3.4	1048	1	US-10-392-234A-18	Sequence 18, Appl
44	63	3.3	317	1	US-10-131-826A-524	Sequence 524, App
45	63	3.3	401	1	US-10-821-234-881	Sequence 881, App

ALIGNMENTS

```
RESULT 1
US-11-135-855-44
; Sequence 44, Application US/11135855
; Publication No. US2005025557A1
; GENERAL INFORMATION:
; APPLICANT: SMITHKLINE BEECHAM CORPORATION
; APPLICANT: SMITHKLINE BEECHAM P.L.C.
; TITLE OF INVENTION: NOVEL COMPOUNDS
; FILE REFERENCE: GP50013
; CURRENT APPLICATION NUMBER: US/11/135,855
; CURRENT FILING DATE: 2005-05-24
; PRIOR APPLICATION NUMBER: US/10/203,708
; PRIOR FILING DATE: 2002-08-13
; PRIOR APPLICATION NUMBER: PCT/US01/04703
; PRIOR FILING DATE: 2001-02-14
; PRIOR APPLICATION NUMBER: 60/182,172
; PRIOR FILING DATE: 2000-02-14
; PRIOR APPLICATION NUMBER: 60/186,084
; PRIOR FILING DATE: 2000-02-29
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 44
; LENGTH: 355
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-135-855-44

Query Match      17.3%; Score 326; DB 7; Length 355;
Best local Similarity 23.1%; Pred. No. 6.1e-25;
Matches 87; Conservative 42; Mismatches 95; Indels 152; Gaps 11;

102 LRGDVEVCAFCVCEIMRWVEGDPAADHRMAPOCFRKQMYNAAAGATVGRDEC-160
1 MGPKDSAKCLHRGPQSHMAAGDPQEQ--RCGPR-----SLG--SPVLGDTCKR 46
-----GASAA--TOPRMFGPVHARSTEAARLATFKDPRRM 196
47 AMHDVQGLIGLRPLTEEBEEBGAATLSRGAFPG-----MGSEELRIASYYDPLTA 101
197 RQPEELAEAGFFYTQSGDKTCFCYDGLKOWESDVPWEQHARFDRCAVQOLYKGRD 256
102 EVPEELIAAAGFHTGHQDKVRCFCYGGIGSWKRGDDPWTEHAKVFPSCFILRSKGRD 161
257 YIKQV-----
162 FVHSVETHSQLLGSVWSATSPRGSQMOWGPADPISPDPDGLWLPDGVGRTGRSPCPG 221
262 -----KSEATA-----ISASBE 273
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Db 222 LRSSLKVPKQVQVAPDLGEGWGRGGLRDBLPMPLEGGQGVGTRRRPVLLGCVSPAEA 281  
QY 274 EGA---ATNDSTGNVAOGEKHLDSKICKICYSEERNVCFPCGHVACAKCALSTDKC 330  
Db 282 QRAMWVLEPFGADVDAQ-LRRLOBERTCKVCIDRANISYVFVCGHLV-CAECPAQLQIC 339  
QY 331 PMCRRTFTNAVRLYFS 346  
Db 340 PICRAPVRSRVRTFLS 355

## RESULT 2

US-11-135-855-45  
; Sequence 45, Application US/11135855  
; Publication No. US2005025557A1  
; GENERAL INFORMATION:  
; APPLICANT: SMITHKLINE BEECHAM CORPORATION  
; APPLICANT: SMITHKLINE BEECHAM P.I.C.  
; TITLE OF INVENTION: NOVEL COMPOUNDS  
; FILE REFERENCE: GP50013  
; CURRENT APPLICATION NUMBER: US/11/135,855  
; CURRENT FILING DATE: 2005-05-24  
; PRIOR APPLICATION NUMBER: US/10/203,708  
; PRIOR FILING DATE: 2002-08-13  
; PRIOR APPLICATION NUMBER: PCT/US01/04703  
; PRIOR FILING DATE: 2001-02-14  
; PRIOR APPLICATION NUMBER: 60/182,172  
; PRIOR FILING DATE: 2000-02-14  
; PRIOR APPLICATION NUMBER: 60/186,084  
; PRIOR FILING DATE: 2000-02-29  
; NUMBER OF SEQ ID NOS: 46  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 45  
; LENGTH: 255  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-11-135-855-45

Query Match 11.9%; Score 225; DB 7; Length 255;  
Best Local Similarity 31.7%; Pred. No. 2.8e-15;  
Matches 53; Conservative 18; Mismatches 52; Indels 44; Gaps 6;  
QY 102 LRGDEVCACFCVETIMRWEGDDPAADHRRMAPQCFVKKQYANAGGATVGRDEC- 160  
Db 1 MGRKDSAKCILHRGPOSHMAAGDPOTQ--RCGPR-----SIG--SPVLGIDTCR 46  
QY 161 -----GASAA--TQPPRMGVPVARYSTEARLATKDMPRRM 136  
Db 47 AMDHVDGQIIGQLRPLTEEEEGAGATLSRGPAFPG---MGSEELRLASFYDMLTA 101  
QY 197 RQREELAEAGFFVTGGQDKTKCFYCDGLKDWESDDVPWEQHARWF 243  
Db 102 EVPELLAAGFPHTHGHQDKVRCFCYGLQSWKRGDDPTEHAKWF 148

## RESULT 3

US-10-821-234-1624  
; Sequence 1624, Application US/10821234  
; Publication No. US20050255114A1  
; GENERAL INFORMATION:  
; APPLICANT: Labate, Ivan  
; APPLICANT: Stache-Crafin, Birgit  
; APPLICANT: Andarmant, Susan  
; APPLICANT: Tang, Y. Tom  
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia  
; FILE REFERENCE: 821A  
; CURRENT APPLICATION NUMBER: US/10/821,234  
; CURRENT FILING DATE: 2004-04-07  
; PRIOR APPLICATION NUMBER: US 60/462,047  
; PRIOR FILING DATE: 2003-04-07  
; NUMBER OF SEQ ID NOS: 1704  
; SOFTWARE: pc\_seq\_genes Version 1.0

; SEQ ID NO 1624  
; LENGTH: 574  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-821-234-1624

Query Match 5.2%; Score 98.5; DB 1; Length 574;  
Best Local Similarity 34.0%; Pred. No. 0.016;  
Matches 18; Conservative 6; Mismatches 24; Indels 5; Gaps 1;

QY 299 CKICYSEERNVCFPCGHVACAKCALSTDK-----CPMCRRTFTNAVRLYFS 346  
Db 521 CTICYHADVTVYITGHNCLCYACGLRLKALHACCPICRPIIDITITS 573

## RESULT 4

US-11-059-982-1  
; Sequence 1, Application US/11059982  
; Publication No. US2005025507A1  
; GENERAL INFORMATION:  
; APPLICANT: Jenkins, Robert B.  
; APPLICANT: Yang, Ping  
; APPLICANT: Thibodeau, Steve  
; APPLICANT: Wang, Liang  
; APPLICANT: Schaid, Daniel  
; TITLE OF INVENTION: CYTOGENETICALLY DETERMINED DIAGNOSIS AND  
; TITLE OF INVENTION: PROGNOSIS OF PROLIFERATIVE DISORDERS  
; FILE REFERENCE: 07039-505001  
; CURRENT APPLICATION NUMBER: US/11/059,982  
; CURRENT FILING DATE: 2005-02-17  
; PRIOR APPLICATION NUMBER: US 60/545,573  
; PRIOR FILING DATE: 2004-02-17  
; NUMBER OF SEQ ID NOS: 50  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 1560  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-11-059-982-1

Query Match 4.7%; Score 88.5; DB 7; Length 1560;  
Best Local Similarity 29.4%; Pred. No. 0.56;  
Matches 37; Conservative 12; Mismatches 48; Indels 29; Gaps 7;  
QY 121 VEGDDPADHR---WAPQCF--VRKQYANAGC---EATAVGDECGASAAATQPPRM 171  
Db 1363 VDHPPPADEBKPLGTAPHCPLRLKTYRENVGSGPAGDEGTPAGARAGS-----PAPL 1417  
QY 172 PCGVHARYSTEARLATTFD--WPRMRQPEELAEAGFFVTGGQDKTKCFYCDGLKDW 229  
Db 1418 PAKVDEATSGLIRELAAVEDELYQRLKGPPEPASA--AAGTGD-----PDW 1464  
QY 230 ESDVDP 235  
Db 1465 EAPGLP 1470

## RESULT 5

US-11-004-057-21  
; Sequence 21, Application US/11004057  
; Publication No. US20050244846A1  
; GENERAL INFORMATION:  
; APPLICANT: Johnson, Gary L.  
; TITLE OF INVENTION: MEK1 PROTEINS AND FRAGMENTS THEREOF FOR USE IN REGULATING  
; TITLE OF INVENTION: APOPTOSIS  
; FILE REFERENCE: CPI-042CPRC  
; CURRENT APPLICATION NUMBER: US/11/004,057  
; CURRENT FILING DATE: 2004-12-02  
; PRIOR APPLICATION NUMBER: US/09/403,075  
; PRIOR FILING DATE: 2000-05-10  
; NUMBER OF SEQ ID NOS: 21  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 21

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OM protein - protein search, using SW model

Run on: November 26, 2005, 17:38:31 ; Search time 77 Seconds  
(without alignments)  
1877.519 Million cell updates/sec

Title: US-10-041-859a-2  
Perfect score: 1887  
Sequence: 1 MELTKYAKKGAATLVMLKN.....TDKCPWCRRFTTNVRLYFS 346

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Maximum Match 0%  
Listing first 45 summaries

Database : Published Applications AA Main:  
1: /cgn2\_6/prodata/1/pubppaa/us07\_PUBCOMB.pep:\*  
2: /cgn2\_6/prodata/1/pubppaa/us08\_PUBCOMB.pep:\*  
3: /cgn2\_6/prodata/1/pubppaa/us09\_PUBCOMB.pep:\*  
4: /cgn2\_6/prodata/1/pubppaa/us10A\_PUBCOMB.pep:\*  
5: /cgn2\_6/prodata/1/pubppaa/us10B\_PUBCOMB.pep:\*  
6: /cgn2\_6/prodata/1/pubppaa/us11\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysts of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1887	100.0	346	4	US-10-041-859-2
2	966	51.2	275	3	US-09-201-936-12
3	966	51.2	275	4	US-10-323-643-9
4	966	51.2	275	4	US-10-600-272-12
5	932.5	49.4	172	4	US-10-041-859-8
6	862	45.7	268	4	US-10-323-643-10
7	846.5	44.9	172	4	US-10-041-859-10
8	831.5	44.1	172	4	US-10-041-859-9
9	767.5	40.7	263	5	US-10-706-635-15
10	759.5	40.2	172	4	US-10-041-859-11
11	719.5	38.1	438	4	US-10-267-502-419
12	719.5	38.1	438	6	US-11-097-143-12366
13	719.5	38.1	438	6	US-11-097-143-12366
14	696.5	36.9	172	4	US-10-041-859-12
15	554.5	29.4	172	4	US-10-041-859-13
16	526.5	27.9	604	4	US-10-232-286-4
17	526.5	27.9	604	4	US-10-141-618-6
18	526.5	27.9	604	4	US-10-366-307-6
19	526.5	27.9	604	4	US-10-730-476A-79
20	526.5	27.9	604	4	US-10-825-282-40
21	526.5	27.9	604	5	US-10-934-717-4
22	526.5	27.9	604	5	US-10-485-225-22
23	526.5	27.9	604	5	US-10-730-476A-79
24	525.5	27.8	600	3	US-09-974-592-12
25	525.5	27.8	600	5	US-10-482-952-1
26	524.5	27.8	604	3	US-09-974-592-6
27	524.5	27.8	604	3	US-09-201-936-6

28	524.5	27.8	604	4	US-10-636-065-221	Sequence 221, App
29	524.5	27.8	604	4	US-10-600-272-6	Sequence 40, Appl
30	517.5	27.4	602	3	US-09-201-936-40	Sequence 6, Appl
31	517.5	27.4	602	4	US-10-636-065-227	Sequence 227, App
32	517.5	27.4	602	4	US-10-600-272-40	Sequence 40, Appl
33	507.5	26.9	618	3	US-09-974-592-8	Sequence 8, Appl
34	507.5	26.9	618	3	US-09-201-936-8	Sequence 8, Appl
35	507.5	26.9	618	3	US-10-636-065-223	Sequence 223, App
36	507.5	26.9	618	4	US-10-600-272-8	Sequence 8, Appl
37	500.5	26.5	498	3	US-09-201-936-13	Sequence 13, Appl
38	500.5	26.5	498	4	US-10-600-272-13	Sequence 13, Appl
39	500.5	26.5	618	4	US-10-153-668-338	Sequence 338, App
40	500.5	26.5	618	4	US-10-207-655-200	Sequence 200, App
41	500.5	26.5	618	4	US-10-232-286-2	Sequence 2, Appl
42	500.5	26.5	618	4	US-10-366-307-4	Sequence 4, Appl
43	500.5	26.5	618	4	US-10-361-270-3	Sequence 3, Appl
44	500.5	26.5	618	4	US-10-260-708-63	Sequence 63, Appl
45	500.5	26.5	618	4	US-10-730-476A-78	Sequence 78, Appl

ALIGNMENTS

RESULT 1					
US-10-041-859-2					
; Sequence 2, Application US/10041859					
; Publication No. US20030049796A1					
; GENERAL INFORMATION:					
; APPLICANT: HUANG, QIHONG					
; APPLICANT: REED, JOHN C.					
; APPLICANT: DEVERAUX, QUINN L.					
; APPLICANT: MAEDA, SUSUMU					
; TITLE OF INVENTION: INHIBITOR OF APOPTOSIS PROTEINS AND NUCLEIC ACIDS AND					
; FILE REFERENCE: 087102/027 2537					
; CURRENT APPLICATION NUMBER: US/10/041,859					
; PRIOR FILING DATE: 2002-01-07					
; PRIOR APPLICATION NUMBER: 60/260,478					
; NUMBER OF SEQ ID NOS: 25					
; SOFTWARE: PatentIn Ver. 2.1					
; SEQ ID NO 2					
; LENGTH: 346					
; TYPE: PRT					
; ORGANISM: Bombyx mori					
US-10-041-859-2					
Query Match					
Best Local Similarity 100.0%; Score 1887; DB 4; Length 346;					
Matches 346; Conservative 0; Mismatches 0; Indels 0; Gaps 0;					
QY	1	MELTKYAKKGAATLVMLKNARDAKRRPTIGPLMSSCSBSTTSTLPSRSSADKTDNDH	60		
DB	1	MELTKYAKKGAATLVMLKNARDAKRRPTIGPLMSSCSBSTTSTLPSRSSADKTDNDH	60		
QY	61	TFNPLDMDPMREERELTTPDQWPVTLPLRBLANGFYVGRGDEVCAFKVEIMRW	120		
DB	61	TFNPLDMDPMREERELTTPDQWPVTLPLRBLANGFYVGRGDEVCAFKVEIMRW	120		
QY	121	VEBDDPAADHRRAPPCPFVFRKMYNAGGEATAVRGDCGSAATOPRMPGPVARYS	180		
DB	121	VEBDDPAADHRRAPPCPFVFRKMYNAGGEATAVRGDCGSAATOPRMPGPVARYS	180		
QY	121	VEBDDPAADHRRAPPCPFVFRKMYNAGGEATAVRGDCGSAATOPRMPGPVARYS	180		
DB	121	VEBDDPAADHRRAPPCPFVFRKMYNAGGEATAVRGDCGSAATOPRMPGPVARYS	180		
QY	181	TEAARLATFPMWRMRKQREBEIAEGFYTGQDITKCFYCDGLKDWSDDVPWEQHA	240		
DB	181	TEAARLATFPMWRMRKQREBEIAEGFYTGQDITKCFYCDGLKDWSDDVPWEQHA	240		
QY	241	RWEDRCAYVOLVGRDYIOKVSEATASBEEOATDSTKNVAOEGEKHLDSDKICK	300		
DB	241	RWEDRCAYVOLVGRDYIOKVSEATASBEEOATDSTKNVAOEGEKHLDSDKICK	300		
QY	301	ICYSERNVCFVCGHVACAKCALSTDKCPMCRRTFTNAVRLYFS	346		
DB	301	ICYSERNVCFVCGHVACAKCALSTDKCPMCRRTFTNAVRLYFS	346		

Db 301 ICYSEERNVCFVPGHVVACAKCALSTDCKPMCRFTTNAVRLYFS 346

## RESULT 2

US-09-201-936-12

Sequence 12, Application US/09201936  
Publication No. US20020187946A1

GENERAL INFORMATION:

APPLICANT: Korneluk, Robert G.

APPLICANT: Mackenzie, Alexander E.

APPLICANT: Baird, Stephen

APPLICANT: Liston, Peter

TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,

TITLE OF INVENTION: PROBES, AND DETECTION METHODS

FILE REFERENCE: 07891/003003

CURRENT APPLICATION NUMBER: US/09/201,936

EARLIER FILING DATE: 1998-12-01

EARLIER APPLICATION NUMBER: 09/011,356

EARLIER FILING DATE: 1998-02-04

EARLIER APPLICATION NUMBER: PCT/IB96/01022

EARLIER FILING DATE: 1996-08-05

EARLIER APPLICATION NUMBER: 08/576,956

EARLIER FILING DATE: 1995-12-22

EARLIER APPLICATION NUMBER: 08/511,485

EARLIER FILING DATE: 1995-08-04

NUMBER OF SEQ ID NOS: 45

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 12

LENGTH: 275

TYPE: PRT

ORGANISM: Cydia pomonella

US-09-201-936-12

Query Match 51.2%; Score 966; DB 3; Length 275;  
Best Local Similarity 59.2%; Pred. No. 1.4e-82;

Matches 171; Conservative 39; Mismatches 55; Indels 24; Gaps 3;

Db 68 MPMRREERLKTFTDQMPVTLTPEQLARNGFYLLGRGDEVCACFCVKEIMRWEGDDPA 127

1 MSDLRLEEVRLNTFEKMPVSLSPETMAKNGFYLLGRSDEVCACFCVKEIMRWEGDDPA 60

Qy 128 ADHRWAPOCFPRKQMYNAGGEATAVGRDECGASAAQ-----PRMGPVARS 180

61 ADHKWAPQCFPVK-----GIDVCGSIYTTNNIQTTHDTITIGPAHPKYA 106

Qy 181 TEAARLATFQDMPRMRKQPEELAEAGFFYTGQGDRTKCFYCDGLKDMESDVPMEQHA 240

107 HEAARVKSFTNMRCKQRPQEMADAGFFYTGIDNTKCFYCDGLKDMESDVPMEQHY 166

Qy 241 RWFDRCAVYQVLYKGRDYIOKVKSEATAI--SASEEQATNDSTKNVAQEGEKHLDDSK 297

167 RWFDRCAVYQVLYKGRDYIOKVKSEATAI--SASEEQATNDSTKNVAQEGEKHLDDSK 226

Qy 298 ICKICVSEERNVCFVPGHVVACAKCALSTDCKPMCRFTTNAVRLYFS 346

227 LCKICVSEERNVCFVPGHVVACAKCALSTDCKPMCRFTTNAVRLYFS 275

Db 227 LCKICVSEERNVCFVPGHVVACAKCALSTDCKPMCRFTTNAVRLYFS 275

Qy 227 LCKICVSEERNVCFVPGHVVACAKCALSTDCKPMCRFTTNAVRLYFS 275

Db 227 LCKICVSEERNVCFVPGHVVACAKCALSTDCKPMCRFTTNAVRLYFS 275

Qy 227 LCKICVSEERNVCFVPGHVVACAKCALSTDCKPMCRFTTNAVRLYFS 275

Db 227 LCKICVSEERNVCFVPGHVVACAKCALSTDCKPMCRFTTNAVRLYFS 275

Qy 227 LCKICVSEERNVCFVPGHVVACAKCALSTDCKPMCRFTTNAVRLYFS 275

Db 227 LCKICVSEERNVCFVPGHVVACAKCALSTDCKPMCRFTTNAVRLYFS 275

Qy 227 LCKICVSEERNVCFVPGHVVACAKCALSTDCKPMCRFTTNAVRLYFS 275

Db 227 LCKICVSEERNVCFVPGHVVACAKCALSTDCKPMCRFTTNAVRLYFS 275

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Db 227 LCKICVSEERNVCFVPGHVVACAKCALSTDCKPMCRFTTNAVRLYFS 275

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Db 227 LCKICVSEERNVCFVPGHVVACAKCALSTDCKPMCRFTTNAVRLYFS 275

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Db 227 LCKICVSEERNVCFVPGHVVACAKCALSTDCKPMCRFTTNAVRLYFS 275

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Db 227 LCKICVSEERNVCFVPGHVVACAKCALSTDCKPMCRFTTNAVRLYFS 275

SOFTWARE: PatentIn version 3.1

SEQ ID NO 9

LENGTH: 275

TYPE: PRT

ORGANISM: Cydia pomonella granulovirus

US-10-523-643-9

Query Match 51.2%; Score 966; DB 4; Length 275;  
Best Local Similarity 59.2%; Pred. No. 1.4e-82;

Matches 171; Conservative 39; Mismatches 55; Indels 24; Gaps 3;

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1 MSDLRLEEVRLNTFEKMPVSLSPETMAKNGFYLLGRSDEVCACFCVKEIMRWEGDDPA 60

Qy 128 ADHRWAPOCFPRKQMYNAGGEATAVGRDECGASAAQ-----PRMGPVARS 180

61 ADHKWAPQCFPVK-----GIDVCGSIYTTNNIQTTHDTITIGPAHPKYA 106

Qy 181 TEAARLATFQDMPRMRKQPEELAEAGFFYTGQGDRTKCFYCDGLKDMESDVPMEQHA 240

107 HEAARVKSFTNMRCKQRPQEMADAGFFYTGIDNTKCFYCDGLKDMESDVPMEQHY 166

Qy 241 RWFDRCAVYQVLYKGRDYIOKVKSEATAI--SASEEQATNDSTKNVAQEGEKHLDDSK 297

167 RWFDRCAVYQVLYKGRDYIOKVKSEATAI--SASEEQATNDSTKNVAQEGEKHLDDSK 226

Qy 298 ICKICVSEERNVCFVPGHVVACAKCALSTDCKPMCRFTTNAVRLYFS 346

227 LCKICVSEERNVCFVPGHVVACAKCALSTDCKPMCRFTTNAVRLYFS 275

Db 227 LCKICVSEERNVCFVPGHVVACAKCALSTDCKPMCRFTTNAVRLYFS 275

Qy 227 LCKICVSEERNVCFVPGHVVACAKCALSTDCKPMCRFTTNAVRLYFS 275

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Qy 227 LCKICVSEERNVCFVPGHVVACAKCALSTDCKPMCRFTTNAVRLYFS 275

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Db 316 PALAPENSVDSSKLCIKICYAERNVCFPCGHVACAKCALAADKCPICRRTFQNAVRLY 375

Qy 345 FS 346

Db 376 FS 377

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RESULT 2
US-08-511-485-12
: Sequence 12, Application US/08511485
: Patent No. 5919912
: GENERAL INFORMATION:
: APPLICANT: Korneiluk, Robert G.
: APPLICANT: Mackenzle, Alexander E.
: APPLICANT: Baird, Stephen
: TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
: TITLE OF INVENTION: PROBES, AND DETECTION METHODS
: NUMBER OF SEQUENCES: 38
: CORRESPONDENCE ADDRESSES:
: ADDRESSEE: Fish & Richardson P.C.
: STREET: 225 Franklin Street
: CITY: Boston
: STATE: MA
: COUNTRY: USA
: ZIP: 02110-2804
: COMPUTER READABLE FORM:
: MEDIUM TYPE: floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/511,485
: FILING DATE: 04-APR-1995
: CLASSIFICATION: 514
: ATTORNEY/AGENT INFORMATION:
: NAME: Clark, Paul T.
: REGISTRATION NUMBER: 30,162
: REFERENCE/DOCKET NUMBER: 07540/002001
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 617/542-5070
: TELEFAX: 617/542-8906
: TELEX: 200154
: INFORMATION FOR SEQ ID NO: 12:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 275 amino acids
: TYPE: amino acid
: STRANDEDNESS: not relevant
: TOPOLOGY: both
: MOLECULE TYPE: protein
:
US-08-511-485-12

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Query Match	51.2%	Score 966;	DB 1;	Length 275;
Best Local Similarity	59.2%;	Pred. No. 2.2e-92;		
Matches 171;	Conservative 39;	Mismatches 55;	Indels 24;	Gaps 3;

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QY      181  TEARLATATFKDMRRMRQKPEELAEAGFFYTQSGDKTCFYCDGGLKDMESDVPWEQHA 240
Db      107  HEARVAVSFNNHMRCKORPEQWADAGFFYTQSGNTKCFYCDGGLKDMEEBDDVPWEQHV 166
QY      241  RWFDRCAVYVGVGRDYIOKVASEATAI---SASEEEOATATDSYTKVANAQGEVHLDDSK 297
Db      167  RWFDRCAVYVGVGRDYIOKVITAEACVLQGEVNTYSTAPVSEIPEITKIKIEKQVYEDSK 226
QY      298  ICKICVSEEBNVGFCPGHVVACAKALSTDKCPMCRGRTFTTNAVFLIYS 346

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Db 227 LCKICVYECIVCFPCGHVVAACAKCALSDYDKCPMKRKITVTSVLKAYES 275

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? GENERAL INFORMATION:
? APPLICANT: Mackenzie, Alex E.
? APPLICANT: Korneluk, Robert G.
? APPLICANT: Mahadevan, Mani S.
? APPLICANT: McLean, Michael
? APPLICANT: Roy, Natalie
? APPLICANT: Ikeda, Joh-e
? TITLE OF INVENTION: Neuronal Apoptosis Inhibitor Protein, Gene Sequence and
? Patent No. 6020127
?
? TITLE OF INVENTION: Mutations Causative of Spinal Muscular Atrophy
?
? FILE REFERENCE: 3477-112, 033477/139214
? CURRENT APPLICATION NUMBER: US/08/836,134A
? CURRENT FILING DATE: 1997-06-20
? NUMBER OF SEQ ID NOS: 23
? SOFTWARE: PatentIn Ver. 2.0
? SEQ ID NO 21
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? LENGTH: 275
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? TYPE: PRT
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? ORGANISM: Cydia pomonella
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? FEATURE:
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? OTHER INFORMATION: Description of Artificial Sequence: PCR primer
?
US-08-836-134-21

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Query Match	51.2%	Score 966;	DB 2;	Length 275;
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Qy	181	TEAARLATPKDPRMRMRKPEELAEAGFFYTGODDKTKCFYCDGGLKDMESDVPWMEQHA	240
		107	HEAARXKSHNMPRCMKORPEOMADAGFFYTGODNTKCFYCDGGLKDMEREDVPWEGHV
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Qy	241	RWFDRCAVQLVKGDYIQYKXSEATL--SASEEQATNTDSKNVAOEGEKNHLDISK	297
		167	RWDFRCAVQLVKGDYQKVIYTEACVLPGEHTVSTAAAPSEIPEYTKLEKPEYQEDSK
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		227	LCKICVCEECICVPCGHVVAACAACALSTDKCMCRKIVTSVLYKLYES
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RESULT 4  
 US-09-493-784-21  
 Sequence 21, Application US/09493784  
 Patent No. 6429011  
 GENERAL INFORMATION:  
 APPLICANT: Mackenzie, Alex E.  
 APPLICANT: Korneljuk, Robert G.  
 APPLICANT: Mahadevan, Mani S.  
 APPLICANT: McLean, Michael  
 APPLICANT: Roy, Natalie  
 APPLICANT: Ikeda, John  
 TITLE OF INVENTION: Neuronal Apoptosis Inhibitor Protein, Gene Sequence and  
 Patent No. 6429011  
 TITLE OF INVENTION: Mutations Causative of Spinal Muscular Atrophy  
 FILE REFERENCE: 3477-112, 033477/113914  
 CURRENT APPLICATION NUMBER: US/09/493,784  
 CURRENT FILING DATE: 2000-01-28  
 PRIOR APPLICATION NUMBER: 08/836,134







GenCore version 5.1.6  
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Run on: November 26, 2005, 16:55:00 ; Search time 6.5 Seconds  
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Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 17545 seqs, 3030971 residues  
Total number of hits satisfying chosen parameters: 35090

Minimum DB seq length: 0  
Maximum DB seq length: 200000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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-TRANS-human40.cdi -LIST=45 -DOCALLIGN=200 -THR SCORE=pct -THR MAX=100  
-THR\_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0  
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-FCGAPOP=6 -FCGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published Applications AA New:\*

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8: /cgn2\_6/ptodata/2/pubppaa/US60\_NEW\_PUB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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1	331	4.9	355	US-11-135-855-44	Sequence 44, Appl
2	230	3.4	255	US-11-135-855-45	Sequence 45, Appl
3	98.5	1.5	574	US-10-821-234-1624	Sequence 1624, Ap
4	95.5	1.4	540	US-10-821-234-1456	Sequence 1456, Ap
5	94.5	1.4	993	US-11-137-465-36	Sequence 36, Appl
6	90	1.3	2432	US-10-821-234-899	Sequence 899, Appl
7	89.5	1.3	428	US-11-074-176-364	Sequence 364, Appl
8	89.5	1.3	1560	US-11-059-982-1	Sequence 1, Appl
9	88.5	1.3	1133	US-10-821-234-1219	Sequence 1219, Ap
10	87	1.3	1493	US-11-004-057-4	Sequence 4, Appl

11	86	1.3	1493	7	US-11-004-057-21	Sequence 21, Appl
12	84.5	1.3	2432	1	US-10-821-234-899	Sequence 899, Appl
13	82.5	1.2	543	1	US-10-689-742-78	Sequence 78, Appl
14	82	1.2	468	1	US-10-793-626-868	Sequence 868, Appl
15	82	1.2	468	1	US-10-793-626-1618	Sequence 1618, Appl
16	82	1.2	1075	1	US-10-821-234-1202	Sequence 1202, Appl
17	79	1.2	339	7	US-11-010-874-3	Sequence 3, Appl
18	79	1.2	1302	7	US-11-004-057-6	Sequence 6, Appl
19	78.5	1.2	259	1	US-10-131-826A-300	Sequence 300, Appl
20	78.5	1.2	259	7	US-11-182-946-2	Sequence 2, Appl
21	78.5	1.2	331	1	US-10-821-234-1650	Sequence 1650, Appl
22	78	1.2	258	7	US-11-054-515-1274	Sequence 1274, Appl
23	78	1.2	514	1	US-10-821-234-998	Sequence 998, Appl
24	78	1.2	579	1	US-10-821-234-1352	Sequence 1352, Appl
25	77.5	1.2	477	1	US-10-131-826A-50	Sequence 50, Appl
26	77.5	1.2	953	7	US-11-057-058-53	Sequence 53, Appl
27	77.5	1.2	953	7	US-11-057-058-57	Sequence 57, Appl
28	77	1.2	2897	7	US-10-499-715-2	Sequence 2, Appl
29	76.5	1.1	138	1	US-10-667-295-176	Sequence 176, Appl
30	76.5	1.1	559	1	US-10-821-234-947	Sequence 947, Appl
31	76.5	1.1	708	1	US-10-821-234-917	Sequence 917, Appl
32	76.5	1.1	895	7	US-11-350-406-2	Sequence 2, Appl
33	76.5	1.1	920	1	US-10-821-234-1129	Sequence 1129, Appl
34	76.5	1.2	1142	7	US-11-044-051-73	Sequence 73, Appl
35	76	1.1	173	1	US-10-667-295-9	Sequence 9, Appl
36	76	1.1	419	1	US-10-821-234-1556	Sequence 1556, Appl
37	76	1.1	525	1	US-10-131-826A-56	Sequence 56, Appl
38	76	1.1	587	1	US-10-925-970-6	Sequence 6, Appl
39	76	1.2	761	1	US-10-485-517-252	Sequence 252, Appl
40	75.5	1.1	328	1	US-10-821-234-1671	Sequence 1671, Appl
41	75.5	1.1	937	7	US-11-057-058-55	Sequence 55, Appl
42	75	1.1	575	1	US-10-131-826A-128	Sequence 128, Appl
43	75	1.1	690	1	US-10-131-826A-306	Sequence 306, Appl
44	74.5	1.1	339	7	US-11-010-874-2	Sequence 2, Appl
45	74.5	1.1	648	1	US-10-793-626-1060	Sequence 1060, Appl

## ALIGNMENTS

RESULT 1  
US-11-135-855-44 Application US/1135855  
; Sequence 44, Application US/1135855  
; Publication No. US2005025557A1  
; GENERAL INFORMATION:  
; APPLICANT: SMITHKLINE BEECHAM CORPORATION  
; APPLICANT: SMITHKLINE BEECHAM P.L.C.  
; TITLE OF INVENTION: NOVEL COMPOUNDS  
; FILE REFERENCE: GP50013  
; CURRENT APPLICATION NUMBER: US/11/135,855  
; CURRENT FILING DATE: 2005-05-24  
; PRIOR APPLICATION NUMBER: US/10/203,708  
; PRIOR FILING DATE: 2002-08-13  
; PRIOR APPLICATION NUMBER: PCT/US01/04703  
; PRIOR FILING DATE: 2001-02-14  
; PRIOR APPLICATION NUMBER: 60/182,172  
; PRIOR FILING DATE: 2000-02-14  
; PRIOR APPLICATION NUMBER: 60/186,084  
; PRIOR FILING DATE: 2000-02-29  
; NUMBER OF SEQ ID NOS: 46  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 44  
; LENGTH: 355  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
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Pred. No.: 5,73e-24 Length: 355  
Score: 331.00 Matches: 97  
Percent Similarity: 36.79% Conservative: 45  
Best Local Similarity: 25.13% Mismatches: 88  
Query Match: 4.95% Gaps: 157  
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Db 57 GlyGlnLeuArgProLeuThrGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 76
QY 704 CAGCTCTCCCGCATGCCCGGCGCCCGTGCACGCGCGGTACTCCACCGGCGCGCGGCTC 763
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Db 77 ArgGlyProAlaPheProGly-----MetGlySerGlnGlnLeuArgLeu 91
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QY 995 GAGGCACTGCG----- 1006
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Db 232 GlnValGlnIleIleArgAspProLeuGlyGlyIleGlyTrrGlyIleArgGlyLeuArgAspPro 251
QY 1006 ----- 1006
Db 252 AspLeuProTrrProIleGlnGlyGlyIleGlyValGlyIleThrPheArgAspProVal 271
QY 1007 -----ATATCTGCTAGGAGAGAGAAACAGAGCC-----GCCACCAATGAT 1045
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 272 LeuLeuGlyGlyIleValSerProAlaGlnIleGlnIleTrrPrrValLeuGlnProPro 291
QY 1046 TCGACTAAGAACTCGCCCAAGAGGCGGAGAAACATTTGATGATCTTAAATATGTAA 1105
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 292 GlyAlaIleArgAspValGlnIleGlnIleGlnIleGlnIleGlnIleGlnIleGlnIle 310
QY 1106 ATATGTTATTTCCAGAGAGCTGTCTGTGTCGCGCGGCGCACGTTGCGGTGCGCTGC 1165
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```

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Db 311 ValCysLeuAspArgAlaValSerIleValPheValProCysGlyHisIleVal---Cys 329
QY 1166 GCCAATGGCGCGCTGTGCGACGACGATGCCGATGTGTGCGAGACGTTTCAAGAAATGCG 1225
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 330 AlaGlnCysAlaIleProGlyLeuGlnIleCysProIleCysArgAlaIleProValArgSerArg 349
QY 1226 GTGCGGCTCTCTTCTCG 1243
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Db 350 ValArgThrPheLeuSer 355

RESULT 2
US-11-135-855-45
; Sequence 45, Application US/11135855
; Publication No. US2005025557A1
; GENERAL INFORMATION:
; APPLICANT: SMITHKLINE BEECHAM CORPORATION
; APPLICANT: SMITHKLINE BEECHAM P.L.C.
; TITLE OF INVENTION: NOVEL COMPOUNDS
; FILE REFERENCE: GP50013
; CURRENT APPLICATION NUMBER: US/11/135,855
; CURRENT FILING DATE: 2005-05-24
; PRIOR APPLICATION NUMBER: US/10/203,708
; PRIOR FILING DATE: 2002-08-13
; PRIOR APPLICATION NUMBER: PCT/US01/04703
; PRIOR FILING DATE: 2001-02-14
; PRIOR APPLICATION NUMBER: 60/182,172
; PRIOR FILING DATE: 2000-02-14
; PRIOR APPLICATION NUMBER: 60/186,084
; PRIOR FILING DATE: 2000-02-29
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: FaSTSeq for Windows Version 3.0
; SEQ ID NO 45
; LENGTH: 255
; TYPE: PRN
; ORGANISM: Homo sapiens
US-11-135-855-45

Alignment Scores:
Pred. No.: 1,7e-14 Length: 255
Score: 230.00 Matches: 63
Percent Similarity: 47.46% Conservative: 21
Best Local Similarity: 35.59% Mismatches: 45
Query Match: 3,44% Indels: 9
Gaps: 9

US-10-041-859A-1 (1-3773) x US-11-135-855-45 (1-255)
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Db 8 LysCysLeuHisIaArgIlePro-----GlnProSerHisIleTrrAlaIaGlyAsp 23
QY 501 TCTACTACCTCGGTCGGGCGGACGAAGTGTCTGTCTTCTGTAAAGTGAATAATTATGA 560
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Db 24 GlyProThrGln-----GluArgCysGlyProArgSerLeu----- 35
QY 561 GGTGGGTGCAAGCGACGATCTCGCCGATCATCGGA----- 599
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 36 ---GlySer-----ProValLeuGlyLeuAspThrCysArgAlaTrr 48
QY 600 -----GATGGGCGCCCGAGTGTCCCTTGTAGCAAAAACAAATGTATGCCACGCTG 650
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 49 AspHisValAspIleGln----- 11Leu 56
QY 651 GGGGAGAGCGGACCGCTGTGCGTAGAGAC-----GAATGTGGGCGCACTGCGGCC--ACG 703
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 57 GlyGlnLeuArgProLeuThrGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 76
QY 704 CAGCTCTCCCGCATGCCCGGCGCCCGTGCACGCGCGGTACTCCACCGGCGCGGCTC 763
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 77 ArgGlyProAlaPheProGly-----MetGlySerGlnGlnLeuArgLeu 91
QY 764 GCCACCTTCMAAGACTGCGCGGACGATATGCGCCAAACCCGAGAACTGCGAGAGGCC 823
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - protein search, using frame\_plus.n2p model

Run on: November 26, 2005, 16:52:30 / Search time 269 Seconds  
(without alignments)  
11720.967 Million cell updates/sec

Title: US-10-041-859A-1  
Perfect score: 6692  
Sequence: 1 cattataacacacttcac.....tcgcgtctactctcgtga 3773

Scoring table: BLOSUM62  
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Ygapop 10.0, Ygapext 0.5  
Fgapop 6.0, Fgapext 7.0  
Delop 6.0, Delext 7.0

Searched: 1867569 segs, 417829326 residues  
Total number of hits satisfying chosen parameters: 3735138

Minimum DB seq length: 0  
Maximum DB seq length: 200000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:  
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-MINMATCH=0.1 -LOOPL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1  
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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database: Published Applications\_AA\_Main.\*  
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3: /cgn2\_6/prodata/1/pubppaa/US09\_PUBCOMB.pep.\*  
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5: /cgn2\_6/prodata/1/pubppaa/US10B\_PUBCOMB.pep.\*  
6: /cgn2\_6/prodata/1/pubppaa/US11\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	966	14.4	275	US-09-201-936-12	Sequence 12, Appl1
3	966	14.4	275	US-10-323-643-9	Sequence 9, Appl1
4	966	14.4	275	US-10-600-272-12	Sequence 12, Appl1
5	932.5	13.9	172	US-10-041-859-8	Sequence 8, Appl1
6	862	12.9	268	US-10-323-643-10	Sequence 10, Appl1
7	846.5	12.6	172	US-10-041-859-10	Sequence 10, Appl1
8	831.5	12.4	172	US-10-041-859-9	Sequence 9, Appl1
9	767.5	11.5	263	US-10-706-635-15	Sequence 15, Appl1
10	759.5	11.3	172	US-10-041-859-11	Sequence 11, Appl1
11	719.5	10.8	438	US-10-267-502-419	Sequence 419, App

12	719.5	10.8	438	6	US-11-097-143-12366	Sequence 12366, A
13	719.5	10.8	438	6	US-11-097-143-28833	Sequence 28833, A
14	696.5	10.4	172	4	US-10-041-859-12	Sequence 12, Appl1
15	554.5	8.3	172	4	US-10-041-859-13	Sequence 13, Appl1
16	526.5	7.9	604	4	US-10-232-286-4	Sequence 4, Appl1
17	526.5	7.9	604	4	US-10-141-618-6	Sequence 6, Appl1
18	526.5	7.9	604	4	US-10-366-307-6	Sequence 6, Appl1
19	526.5	7.9	604	4	US-10-730-476A-79	Sequence 79, Appl1
20	526.5	7.9	604	4	US-10-825-282-40	Sequence 40, Appl1
21	526.5	7.9	604	5	US-10-934-717-4	Sequence 4, Appl1
22	526.5	7.9	604	5	US-10-485-225-22	Sequence 22, Appl1
23	526.5	7.9	604	5	US-10-730-476A-79	Sequence 79, Appl1
24	525.5	7.9	600	3	US-09-974-592-12	Sequence 12, Appl1
25	525.5	7.9	600	5	US-10-482-952-1	Sequence 1, Appl1
26	524.5	7.8	604	3	US-09-974-592-6	Sequence 6, Appl1
27	524.5	7.8	604	3	US-09-201-936-6	Sequence 6, Appl1
28	524.5	7.8	604	4	US-10-636-065-221	Sequence 221, App
29	524.5	7.8	604	4	US-10-600-272-6	Sequence 6, Appl1
30	517.5	7.7	602	3	US-09-201-936-40	Sequence 40, Appl1
31	517.5	7.7	602	4	US-10-636-065-227	Sequence 227, App
32	517.5	7.7	602	4	US-10-600-272-40	Sequence 40, Appl1
33	507.5	7.6	618	3	US-09-974-592-8	Sequence 8, Appl1
34	507.5	7.6	618	3	US-09-201-936-8	Sequence 8, Appl1
35	507.5	7.6	618	4	US-10-636-065-223	Sequence 223, App
36	507.5	7.6	618	4	US-10-600-272-8	Sequence 8, Appl1
37	500.5	7.5	498	3	US-09-201-936-13	Sequence 13, Appl1
38	500.5	7.5	498	4	US-10-600-272-13	Sequence 13, Appl1
39	500.5	7.5	618	4	US-10-153-668-338	Sequence 338, App
40	500.5	7.5	618	4	US-10-207-655-200	Sequence 200, App
41	500.5	7.5	618	4	US-10-232-286-2	Sequence 2, Appl1
42	500.5	7.5	618	4	US-10-366-307-4	Sequence 4, Appl1
43	500.5	7.5	618	4	US-10-361-270-3	Sequence 3, Appl1
44	500.5	7.5	618	4	US-10-260-708-63	Sequence 63, Appl1
45	500.5	7.5	618	4	US-10-730-476A-78	Sequence 78, Appl1

## ALIGNMENTS

RESULT 1  
US-10-041-859-2  
; Sequence 2, Application US/10041859  
; Publication No. US20030049796A1  
; GENERAL INFORMATION:  
; APPLICANT: HUANG, OIHONG  
; APPLICANT: REED, JOHN C.  
; APPLICANT: DEVERAUX, QUINN L.  
; APPLICANT: MAEDA, SUSUNU  
; TITLE OF INVENTION: INHIBITOR OF APOPTOSIS PROTEINS AND NUCLEIC ACIDS AND  
; FILE REFERENCE: 087102/027 2537  
; CURRENT APPLICATION NUMBER: US/10/041, 859  
; PRIOR FILING DATE: 2002-01-07  
; PRIOR APPLICATION NUMBER: 60/260, 478  
; NUMBER OF SEQ ID NOS: 25  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 2  
; LENGTH: 346  
; TYPE: PRT  
; ORGANISM: Bombyx mori  
US-10-041-859-2

Alignment Scores:  
Pred. No.: 3.14e-166  
Score: 1887.00  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 28.20%  
DB: 4  
Gaps: 0

US-10-041-859A-1 (1-3773) x US-10-041-859-2 (1-346)  
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21 AlaArgAspAlaLysMetArgProPheIleGlyProLeuMetLeuSerSerCySGluser 40  
326 TCACAGCATCCACTCCCGTCACTTCCTGCTCGTCACTGATATAACGATTAATCAAGAC 385  
41 SerThrThrSerThrLeuProSerProSerSerSerAlaAspYsthrAspAsnHisAsp 60  
386 ACATTGAACCTTCCTCTGATATGCCGAGATCGTCGTGAAGAAGAACTCGAAACCA 445  
61 ThrPheAsnThrLeuProAspMetProAspMetArgTgGluGluGluValArgLeuLysThr 80  
446 TTTCATCAGTGGCCGCTTACGTTTGTGACCCGGAACAATTTGGCCCGCAACGAGATTCTAC 505  
81 PheAspGlnThrProValAlaThrPheLeuThrProGluGluLeuAlaArgAsnGlyPheNyr 100  
506 TACCTCGTGGCGGCGACGAAAGTGCTGTCTTCTGTGAAGGTAGAATATGAGGTGG 565  
101 TyrLeuGlyArgGlyAspGluValCySGySAlaPheCySylValGluIleMetAcgTyr 120  
566 GTCCGAGGCGGACGATCCTCGCGCATCATCGGAGATGGCGCCGACGTGCTCCCTTGTGA 625  
121 ValGluGlyAspAspProAlaAlaAspHisArgArgTyrAlaProGluInCySProPheVal 140  
626 CCAAAAACAATGTATGCAACGCTGGGGGAGAGCGCACCGCTGCTGGTAGAGACGATGT 685  
141 ArgLysGluMetCysrAlaAsnAlaGlyGlyGluAlaThrAlaValGlyAspAspGluCyS 160  
686 GGGGCGACGTGGCGGCGACGACGCTCCCGCATGCGCGGCGCGCTGCACGCGCGTACTCC 745  
161 GlyAlaSerAlaAlaThrGlnProProArgMetProGlyProValHisAlaAspGlySer 180  
746 ACCGAGGCGCGGCGCTCCGACCTTCAAGACGTGGCGGAGAGATGAGCGCAAAACCC 805  
181 ThrGluAlaAlaArgLeuAlaThrPheLysAspTyrProArgArgMetAcgGlnLysPro 200  
806 GAGGAACGTGGCAGAGGCGCGATCTTCTATACAGGCGCAAGGTGACAAACGAATGCTTC 865  
201 GluGluLeuAlaGluAlaGlyPhePheNyrThrGlyGluGlyAspYsthrLysCySPh 220  
866 TATTCGACGCGAGGCGTAAAGATTGGGAAAGCGATGACGTTCCGTGGGAAACGACGCGC 925  
221 TyrCySAspGlyGlyLeuLysAspTyrGluSerAspValProTyrGluGlnHisAla 240  
926 AAGATGGTTGACCGCGCTGCGCTACGTCGCAATTTGGTGAAGAGACGTACATTCAGAAAG 985  
241 ArgTyrPheAspArgCySAlaTyrValGluLeuValLysGlyArgAspTyrIleGlnLys 260  
986 GTGAAGTCGGAGGCGCATGCGATATCTGTACGGAAGAAAGACAGCGCGCACCAATGAT 1045  
261 ValLysSerGluAlaThrAlaIleSerAlaSerGluGluGluGlnAlaAlaThrAspAs 280  
1046 TCGACATTAAGAACTGCCCAAGAGGCGGAGAAACATTTGGATGACTTAAATATGTAA 1105  
281 SerThrLysAsnValAlaGlnGluGlyGluLysHisLeuAspAspSerLysIleCySlys 300  
1106 ATATGTTATTCGAGAGAGGTAAAGTGTGCTGTGTCGCGCGGCGCACGTCGTGGGTGTC 1165  
301 IleCySArgSerGluGluArgAsnValCySAspValProCySgluHisValAlaAlaCyS 320  
1166 GCCAAGTGGCGGCTGTGCAAGCAAGTGGCCGATGTCGCAAGACGTTCAAGAAATGCG 1225  
321 AlaLysCySAlaLeuSerThrAspLysCySArgMetCySArgArgThrPheThrAspAla 340  
1226 GTTCGGGCTCTACTTCTCG 1243  
341 ValArgLeuLysPheSer 346

RESULT 2  
US-09-201-936-12

Sequence 12, Application US/09201936  
Publication No. US20020187946A1  
GENERAL INFORMATION:  
APPLICANT: Korneluk, Robert G.  
APPLICANT: Mackenzie, Alexander E.  
APPLICANT: Baird, Stephen  
APPLICANT: Liston, Peter  
TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,  
TITLE OF INVENTION: PROBES, AND DETECTION METHODS  
FILE REFERENCE: 07891/003003  
CURRENT APPLICATION NUMBER: US/09/201,936  
EARLIER APPLICATION NUMBER: 09/011,356  
EARLIER FILING DATE: 1998-02-04  
EARLIER APPLICATION NUMBER: PCT/IB96/01022  
EARLIER FILING DATE: 1996-08-05  
EARLIER APPLICATION NUMBER: 08/576,956  
EARLIER FILING DATE: 1995-12-22  
EARLIER APPLICATION NUMBER: 08/511,485  
NUMBER OF SEQ ID NOS: 45  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 12  
LENGTH: 275  
TYPE: PRT  
ORGANISM: *Cydia pomonella*  
US-09-201-936-12  
Alignment Scores:  
Pred. No.: 1,548-80 Length: 275  
Score: 966.00 Matches: 171  
Percent Similarity: 72.66% Conservative: 39  
Best Local Similarity: 59.17% Mismatches: 55  
Query Match: 14.44% Indels: 24  
Gaps: 3  
US-10-041-859A-1 (1-3773) x US-09-201-936-12 (1-275)  
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1 MetSerAspLeuArgLeuGluGluValAlaArgLeuAsnThrPheGluLysTyrProValSer 20  
467 TTTTTCACGCGGAGACAAATTTGGCCGCAACGATTTACTACTTCGCTGCGGCGACGAA 526  
21 PheLeuSerProGluThrMetAlaLysAsnGlyPheNyrTyrluGlyArgSerAspGlu 40  
527 GTGTGCTGTCCTTCTGTGAAGTAAATTAAGAGGTGGTGAAGGCGACGATCCTGCG 586  
41 ValArgCySAlaPheCysLysValGluIleMetArgTyrLysGluGlyLysAspProAla 60  
587 GCCGATCATCGAGATGGCGCGCCGACGTCCCTTTGTACGAAACCAATGTATGCCAAC 646  
61 AlaAspHisLysLysTyrAlaProGlnCySProPheValLys----- 74  
647 GCTGGGGAGAGGCGACCGCTGCGGTAGAGACGAATTTGGGCGCATGCGCGCACGCG 706  
75 -----GlyIleAspValCySgluSerIleValThrThrAsn 86  
707 -----CCTCCGCGATGCCCGCGCGGTGACGCGGCTACTCC 745  
87 AsnIleGluAsnThrThrThrHisAspThrIleIleGlyProAlaHisProLysTyrAla 106  
746 ACCGAGGCGCGCGCTCGCCACCTTCAAGACGATGGCCGAGACGTATGGCGCAAAACCC 805  
107 HisGluAlaAlaArgValLysSerPheHisAsnTyrProArgCySmetLysGlnArgPro 126  
806 GAGGAACGTGGCAGAGGCGCGATTTCTTATACAGGCGCAAGGTGACAAACGAATGCTTC 865  
127 GluGlnMetAlaAspAlaGlyPhePheNyrThrGlyTyrGlyAspAsnThrLysCySPh 146  
866 TATTCGACGAGGCGCTAAAGATTGGGAAAGCAATGAGCTTCGCTGGGAAACGACGCGC 925  
147 TyrCySAspGlyGlyLeuLysAspTyrGluProGluAspValProTyrGluGlnHisVal 166





GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - protein search, using frame\_plus\_n2p model

Run on: November 26, 2005, 15:36:38 / Search time 430.5 Seconds  
(without alignments)  
12366.821 Million cell updates/sec

Title: US-10-041-859A-1

Perfect score: 6692  
Sequence: 1 cattataaactcattcac.....tcgcgctcactctcgtga 3773

Scoring table: BLOSUM62  
Xgapop 10.0, Xgapext 0.5  
Ygapop 10.0, Ygapext 0.5  
Fgapop 6.0, Fgapext 7.0  
Delop 6.0, Delext 7.0

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 4332886

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:

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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database: uniprot\_05.80.\*  
1: uniprot\_sprot.\*  
2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	1866	27.9	346	Q81831_BOMMO	Q81831 Bombyx mori
3	1333.5	19.9	379	Q9U492_TRINI	Q9U492 trichoplusi
4	1319	19.7	377	Q9NU07_SPOFR	Q9NU07 spodoptera
5	966	14.4	275	1 IAP GVC	Q61476 cydia pomon
6	937	14.0	287	2 O6E7G7_NPVAG	Q6E7G7 artocaria
7	890.5	13.3	280	2 O6E7V9_NPVCD	Q6E7V9 choristoneu
8	879	13.1	263	2 Q80S54_NPVHC	Q80S54 hyphantia
9	876	13.1	281	2 Q9YN18_NPVCF	Q9YN18 choristoneu
10	873	13.0	261	2 Q9QES9_NPVCP	Q9QES9 epidiyas po
11	873	13.0	276	2 Q89744_NPVBS	Q89744 buziyas sup
12	862	12.9	268	1 IAP3_NPVOP	PA1437 oryctia psen
13	782	11.7	264	2 Q9EN57_AMEPV	Q9EN57 amacta moo
14	747.5	11.2	255	2 Q7TS51_GVCL	Q7TS51 cryptophleb
15	728	10.9	313	2 Q9J827_9NUCL	Q9J827 spodoptera
16	719.5	10.8	438	1 IAP1_DROME	Q43106 drosophila

17	701	10.5	403	2 Q8WRD9_AEDTR	Q8WRD9 aedes trise
18	684	10.2	401	2 Q6Q507_AEDAE	Q6Q507 aedes aegy
19	684	10.1	402	2 Q8T621_AEDAL	Q8T621 aedes albop
20	662	9.9	285	2 Q8JM16_9NUCL	Q8JM16 mamestra co
21	653	9.8	276	2 Q71A73_9NUCL	Q71A73 mamestra co
22	653	9.8	276	2 Q8QJ95_NPVVC	Q8QJ95 mamestra co
23	635	9.5	283	2 Q80LKH_NPVVC	Q80LKH adoxophyes
24	623.5	9.3	278	2 Q4KT41_9NUCL	Q4KT41 chrysodeixi
25	573	8.6	254	2 Q7T9S6_GVAV	Q7T9S6 adoxophyes
26	550	8.2	414	2 Q4T660_TETNG	Q4T660 tetrodon n
27	544.5	8.1	269	2 Q6QXJ6_GVAS	Q6QXJ6 agrotis beg
28	542	8.1	358	1 PIAP_PIG	Q62640 sus scrofa
29	538.5	8.0	304	2 Q5TWU6_AMOGA	Q5TWU6 anopheles g
30	532.5	8.0	268	2 Q9E232_9NUCL	Q9E232 helioverpa
31	530.5	7.9	401	2 Q8JHV9_XENLA	Q8JHV9 xenopus lae
32	530	7.9	186	2 Q7QJ55_ANOGA	Q7QJ55 anopheles g
33	529.5	7.9	268	2 Q7TLM6_9NUCL	Q7TLM6 helioverpa
34	529.5	7.9	268	2 Q91F18_9NUCL	Q91F18 helioverpa
35	528.5	7.9	602	2 Q9ESB9_RAT	Q9ESB9 rattus norv
36	528.5	7.9	602	2 Q5XIM4_RAT	Q5XIM4 rattus norv
37	526.5	7.9	604	1 BIRC3_HUMAN	Q13489 homo sapien
38	526	7.9	604	2 Q6DDY3_XENLA	Q6DDY3 xenopus lae
39	525.5	7.9	600	1 BIRC3_MOUSE	Q08863 mus musculu
40	522	7.8	604	2 Q6GLD7_XENTR	Q6GLD7 xenopus tro
41	516.5	7.7	616	2 Q8Q4E2_ICTPU	Q8Q4E2 ictalurus p
42	514	7.7	628	2 Q8UMD2_BRARE	Q8UMD2 brachydanio
43	514	7.7	647	2 Q7TOK2_BRARE	Q7TOK2 brachydanio
44	514	7.7	654	2 Q6ZM93_BRARE	Q6ZM93 brachydanio
45	511.5	7.6	639	2 Q4SPS0_TETNG	Q4SPS0 tetrodon n

# ALIGNMENTS

RESULT 1  
Q96878\_BOMMO Q96878\_BOMMO PRELIMINARY; PRT; 346 AA.  
AC Q96878;  
DT 01-DEC-2001 (TREMBLrel. 19, Created)  
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)  
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)  
DE Inhibitor of apoptosis protein.  
GN Name=IAP;  
OS Bombyx mori (Silk moth).  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Bombycoidea;  
OC Bombycidae; Bombyx.  
OX NCBI\_TaxId=7091;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RX MEDLINE=21240184; Pubmed=11341966; DOI=10.1016/S0167-4889(00)00105-1;  
RA Huang Q., Deveraux Q.L., Maeda S., Stennicke H.R., Hammock B.D.,  
Reed J.C.;  
RT "Cloning and characterization of an inhibitor of apoptosis protein  
(IAP) from Bombyx mori.";  
RL Biochim. Biophys. Acta 1499:191-198(2001).  
DR EMBL: AF281073; AKS7560.1; -, mRNA.  
DR HSSP: Q24306; 1040.  
DR GO: GO:0000151; C:ubiquitin ligase complex; IEA.  
DR GO: GO:0004842; F:ubiquitin-protein ligase activity; IEA.  
DR GO: GO:0008270; F:zinc ion binding; IEA.  
DR GO: GO:0006916; P:anti-apoptosis; IEA.  
DR GO: GO:0016567; P:protein ubiquitination; IEA.  
DR InterPro: IPR001370; Prot\_inh\_132\_IAP.  
DR InterPro: IPR001841; Znf\_fing.  
DR Pfam: PF00653; BIR; 2.  
DR SMART: SM00238; BIR; 2.  
DR SMART: SM00184; RING; 1.  
DR PROSITE: PS01282; BIR\_REPEAT\_1; 2.  
DR PROSITE: PSS0143; BIR\_REPEAT\_2; 2.  
DR PROSITE: PSS0089; ZF\_RING\_2; 1.  
SQ SEQUENCE 346 AA; 38942 MW; 6CFC6C6468894C69 CRC64;

Alignment Scores:

Pred. No.:	3 29e-155	Length:	346
Score:	1887.00	Matches:	346
Percent Similarity:	100.00%	Conservative:	0
Best local Similarity:	100.00%	Mismatches:	0
Query Match:	28.20%	Indels:	0
DB:	2	Gaps:	0

US-10-041-859A-1 (1-3773) x Q968T8\_BOMMO (1-346)

QY	206	ATGGAGTTGACAAAGTGGCTTAAATGAGAGCTGGCCGACGTTGGTGTATGTTAAATAAT	265
Db	1	MetGluLeuThrIleValAlaIleAspAsnGlyAlaAlaIleThrLeuValMetLeuIleuAspAn	20
QY	266	GCGCGGGATGCAAAATGCGACCTTTTCATTTGGTCGGCTCATGTTATCTGTGTGAGTCT	325
Db	21	AlaIArgAspAlaIleuMetCysArgProPheIleGlyProLeuMetLeuSerCysGluSer	40
QY	326	TCAACGACATCCACACTCCCGTCACCTTGTGTGTACGCTGATTTAAACGGATATACGAC	385
Db	41	SeThrTrpIleSerThrLeuProSerProSerSerSerAlaAspIleThrAspAsnIleAsp	60
QY	486	ACATTCACCTTCCTTCGTATATGCCCCGACATGCGTCGTAAGAGAGAAAGTCTGAAATAA	445
Db	61	ThrPheAsnPheLeuProAspMetProAspMetCysArgGluGluIleuArgLeuIleuSer	80
QY	446	TTTGATCAGTGGCCCGCTTACGTTTTTTGACGCCGGAACAATTGGCCGCAACGATTTCTAC	505
Db	81	PheAspGlnTrpProValThrPheLeuThrProGluGluLeuAlaArgAsnGlyPheTyr	100
QY	506	TACCTCCGTCGGGGGACGAAATGTGTCTGTCTTTCTGTAAAGTAAATTTATGAGCTGG	565
Db	101	TyrLeuGlyArgGlyAspGluValCysCysAlaPheCysAlaValGluIleMetArgTrp	120
QY	566	GTCCGAAGCGACGATCTCCGCCCGCATCTCCGAGATGTGGCGCCCGACGTCCTCTTGA	625
Db	121	ValGluGlyAspAspProAlaAlaAspAlaAspArgTrpAlaProGluCysProPheVal	140
QY	626	CGAAACAATATGTATGCCACGCTGGGGGAGAGCGCACCGCTGTCCGTAGAGACGAATGT	685
Db	141	ArgIleuGlnMetTyrAlaAsnAlaGlyGluGluIleuAlaThrAlaValGlyArgAspGlyCys	160
QY	686	GGGGCGAATGGGGCCACGACGCTTCCCGCATGCCCCGGCCCGCTGACGCGGGTACTCC	745
Db	161	GlyAlaSerAlaAlaIleThrGlnProProArgMetProGlyProValAlaAlaArgTyrSer	180
QY	746	ACCGAGCGCGCGGCTCGCCACTTCAAGAACTGGCGCAGACGTATGGCGCAAAAACCC	805
Db	181	ThrGluAlaAlaArgLeuAlaThrPheLeuAspTrpProArgArgMetCysGlnIleuAsp	200
QY	806	GAGGAACGTGCAGAGGCGCGATTTCTTATACAGGCGCAAGGTACAAAAGAAATGCTTTC	865
Db	201	GluGluLeuAlaGluAlaGlyPhePheTyrThrGlyGlnGlyAspArgTyrThrIleCysPhe	220
QY	866	TATTGCCACGGAGGCTTAAGAATTGGGAAACGATGACGTTCCGTGGGAAACAGCAGCC	925
Db	221	TyrCysAspArgGlyGlyLeuIleuAspTrpGluSerAspAspValProTrpGluGlnIleAla	240
QY	926	AGATGGCTTCGACCGCTGCGCGCTACGCGAAATTGGGAAAGGACGTACATTCAGAAAG	985
Db	241	ArgTrpPheAspArgCysAlaTyrValGlnLeuValIleGlyAlaArgAspTyrIleGlnIleu	260
QY	986	GTGAAGTGCAGAGCCACTGCATATCTGCTACGGAAGAAGAACAGGCGCCGACCATGAT	1045
Db	261	ValIleuSerGluAlaThrAlaIleSerAlaSerGluGluGluGlnAlaAlaThrAsnAsp	280
QY	1046	TCGACATAAGACGTGCGCCCAAGAGGGCGGAAACATTGGATGACTTTAAATATGTAA	1105
Db	281	SeThrTrpLeuAsnValAlaGlnGluGlyGlyIleuValLeuAspAspSerTyrIleCysIleu	300
QY	1106	ATATGTTATTTCCGAGGAGCGTAAAGTGTGCTTCGTGCGCTGCGCGGCGGACGCTGGCTG	1165
Db	301	IleCysTyrSerGluGluArgAsnAlaCysPheValProCysGlyAlaValAlaAlaCys	320

[illegible]

## RESULT 2

ID Q8IS31\_BOMMO PRELIMINARY; PRT; 346 AA.

DT	01-MAR-2003 (TREMBlrel, 23, Created)
DE	01-MAR-2003 (TREMBlrel, 23, Created)

DT 01-OCT-2003 (Tremblé et al., 2003)  
 DE Inhibitor of anionois protein

05 Bombyx mori (Silk moth)  
06 Eukaryota: Metazoa: Arthropoda: Insecta: Lepidoptera: Bombyx mori

0C Bombycidae; Bombyx.

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RA Yang G., Wang L., W

DR EMBL; AY155274; AAN46650.1; -; mRNA.  
DB HSSD; 024206; 1040

DR GO: GO:0004842: E:ubiquitin-protein ligase activity

DR GO: GO:0006270; F: zinc ion binding; IEA.  
DR GO: GO:0006916; P: anti-apoptosis; IEA.

DR InterPro; IPR001370; Prot\_inh\_I32\_IAP.

DR Pfam; PF00653; BIR; 2.

DR SMART; SM00184; RING; 1.

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DR PROSITE; PSS0143; BIR_REPEAT_2; 2.
DR PROSITE; PS50089; 2F_PING_2; 1
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SEQUENCE 340 AA; 36843 MW; 3420EB/2F20A0400 CAC04;

Pred. No.:

Percent Similarity: 99.13% Conservative: 0

Query Match:	27.88%	Indels:	0
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FILE NO. 041 0500 1 (1 3773) - OCTOBER 1960 / 1 345

206 ATGGAATTGACGAAAGTTGCTAAAAATGAGCGTCGCGCCACGTTGGTGATGTTAAAAAAT 265

Db 1 MetGluLeuThrIysValAlaIysAsnGlyAlaAlaAlaThrLeuValMetLeuIysAsn 20

266 GCGGGATGCAAAATGCGACCTTTCATTGGTCCGCTCATGTTATCCTCGTGAGTCT 325

Db 21 AlaArgAspAlaLysMetArgProPheIleGlyProLeuMetLeuSerSerCysGluSer 40

326 TCAACGACATCCACACTCCCGTCACCTTCGTGTCAGCTGATAAACGGATAATCAGCAC 385

Db 41 SerThrThrSerThrLeuProSerProSerSerSerAlaSerLysThrAspValHisVal 60

386 ACAATCAACTTCCATCCGACATGCGTGGATGAGGAAATGCTGATGAC 443

22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45 46 47 48 49 50 51 52 53 54 55 56 57 58 59 60 61 62 63 64 65 66 67 68 69 70 71 72 73 74 75 76 77 78 79 80 81 82 83 84 85 86 87 88 89 90 91 92 93 94 95 96 97 98 99 100 101 102 103 104 105 106 107 108 109 110 111 112 113 114 115 116 117 118 119 120 121 122 123 124 125 126 127 128 129 130 131 132 133 134 135 136 137 138 139 140 141 142 143 144 145 146 147 148 149 150 151 152 153 154 155 156 157 158 159 160 161 162 163 164 165 166 167 168 169 170 171 172 173 174 175 176 177 178 179 180 181 182 183 184 185 186 187 188 189 190 191 192 193 194 195 196 197 198 199 200 201 202 203 204 205 206 207 208 209 210 211 212 213 214 215 216 217 218 219 220 221 222 223 224 225 226 227 228 229 230 231 232 233 234 235 236 237 238 239 240 241 242 243 244 245 246 247 248 249 250 251 252 253 254 255 256 257 258 259 260 261 262 263 264 265 266 267 268 269 270 271 272 273 274 275 276 277 278 279 280 281 282 283 284 285 286 287 288 289 290 291 292 293 294 295 296 297 298 299 300 301 302 303 304 305 306 307 308 309 310 311 312 313 314 315 316 317 318 319 320 321 322 323 324 325 326 327 328 329 330 331 332 333 334 335 336 337 338 339 340 341 342 343 344 345 346 347 348 349 350 351 352 353 354 355 356 357 358 359 360 361 362 363 364 365 366 367 368 369 370 371 372 373 374 375 376 377 378 379 380 381 382 383 384 385 386 387 388 389 390 391 392 393 394 395 396 397 398 399 400 401 402 403 404 405 406 407 408 409 410 411 412 413 414 415 416 417 418 419 420 421 422 423 424 425 426 427 428 429 430 431 432 433 434 435 436 437 438 439 440 441 442 443 444 445 446 447 448 449 450 451 452 453 454 455 456 457 458 459 460 461 462 463 464 465 466 467 468 469 470 471 472 473 474 475 476 477 478 479 480 481 482 483 484 485 486 487 488 489 490 491 492 493 494 495 496 497 498 499 500 501 502 503 504 505 506 507 508 509 510 511 512 513 514 515 516 517 518 519 520 521 522 523 524 525 526 527 528 529 530 531 532 533 534 535 536 537 538 539 540 541 542 543 544 545 546 547 548 549 550 551 552 553 554 555 556 557 558 559 560 561 562 563 564 565 566 567 568 569 570 571 572 573 574 575 576 577 578 579 580 581 582 583 584 585 586 587 588 589 590 591 592 593 594 595 596 597 598 599 600 601 602 603 604 605 606 607 608 609 610 611 612 613 614 615 616 617 618 619 620 621 622 623 624 625 626 627 628 629 630 631 632 633 634 635 636 637 638 639 640 641 642 643 644 645 646 647 648 649 650 651 652 653 654 655 656 657 658 659 660 661 662 663 664 665 666 667 668 669 670 671 672 673 674 675 676 677 678 679 680 681 682 683 684 685 686 687 688 689 690 691 692 693 694 695 696 697 698 699 700 701 702 703 704 705 706 707 708 709 710 711 712 713 714 715 716 717 718 719 720 721 722 723 724 725 726 727 728 729 730 731 732 733 734 735 736 737 738 739 740 741 742 743 744 745 746 747 748 749 750 751 752 753 754 755 756 757 758 759 760 761 762 763 764 765 766 767 768 769 770 771 772 773 774 775 776 777 778 779 780 781 782 783 784 785 786 787 788 789 790 791 792 793 794 795 796 797 798 799 800 801 802 803 804 805 806 807 808 809 810 811 812 813 814 815 816 817 818 819 820 821 822 823 824 825 826 827 828 829 830 831 832 833 834 835 836 837 838 839 840 841 842 843 844 845 846 847 848 849 850 851 852 853 854 855 856 857 858 859 860 861 862 863 864 865 866 867 868 869 870 871 872 873 874 875 876 877 878 879 880 881 882 883 884 885 886 887 888 889 890 891 892 893 894 895 896 897 898 899 900 901 902 903 904 905 906 907 908 909 910 911 912 913 914 915 916 917 918 919 920 921 922 923 924 925 926 927 928 929 930 931 932 933 934 935 936 937 938 939 940 941 942 943 944 945 946 947 948 949 950 951 952 953 954 955 956 957 958 959 960 961 962 963 964 965 966 967 968 969 970 971 972 973 974 975 976 977 978 979 980 981 982 983 984 985 986 987 988 989 990 991 992 993 994 995 996 997 998 999 1000 1001 1002 1003 1004 1005 1006 1007 1008 1009 1010 1011 1012 1013 1014 1015 1016 1017 1018 1019 1020 1021 1022 1023 1024 1025 1026 1027 1028 1029 1030 1031 1032 1033 1034 1035 1036 1037 1038 1039 1040 1041 1042 1043 1044 1045 1046 1047 1048 1049 1050 1051

100

[illegible]



GenCore version 5.1.6  
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OM nucleic - protein search, using frame\_plus\_n2p model

Run on: November 26, 2005, 15:37:23 ; Search time 64.5 Seconds  
(without alignments)  
11256.615 Million cell updates/sec

Title: US-10-041-859A-1  
Perfect score: 6692  
Sequence: 1 cattataaactcattcac.....tgcgcctactctcgtga 3773

Scoring table:  
BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 263416 seqs, 96216763 residues  
Total number of hits satisfying chosen parameters: 566832

Minimum DB seq length: 0  
Maximum DB seq length: 200000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:  
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-DB=PIR -QFMT=fastan -SUFFIX=n2p.rpr -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0  
-UNITS-bits -START=1 -END=1 -MATRIX=blomsum62 -TRANS=human40.cdi -LIST=45  
-DOCALLIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL  
-OUTFMT=pro -NOR=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000  
-USFR=US1004159.qccn 1.1.94 @runat\_23112005\_100312\_11868 -NCPU=6 -ICPU=3  
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-DEV TIMEOUT=120 -MAIN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : PIR\_80.\*  
1: pir1.\*  
2: pir2.\*  
3: pir3.\*  
4: pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	966	14.4	275	A45679	inhibitor-of-apopt
2	862	12.9	268	T10304	apoptosis-inhibiti
3	862	12.9	268	A53989	apoptosis-inhibiti
4	542	8.1	358	JC5964	apoptosis-inhibito
5	524.5	7.8	604	S68449	apoptosis-inhibito
6	507.5	7.6	618	S68450	apoptosis-inhibito
7	501	7.5	497	S69545	apoptosis-inhibito
8	497.5	7.4	496	S69542	apoptosis-inhibito
9	497.5	7.4	497	S69544	apoptosis-inhibito
10	381.5	5.7	292	T41772	IAP1 orf27 - Bomby
11	378	5.6	286	D36828	orf13 protein - Au
12	369.5	5.5	275	T10310	apoptosis-inhibiti
13	367.5	5.5	298	JC7568	Kidney inhibitor o
14	312	4.7	1447	T42628	neuronal apoptosis

15	302.5	4.5	1232	A55478	neuronal apoptosis
16	253	3.8	208	T03183	probable apoptosis
17	252.5	3.8	150	T28409	ORF MSV248 probabl
18	232	3.5	234	T30427	probable apoptosis
19	222.5	3.3	155	T30489	apoptosis-inhibito
20	220.5	3.3	997	T43523	cutl1 protein - fi
21	171.5	2.6	308	T37474	apoptosis-inhibito
22	169.5	2.5	329	T28403	ORF MSV242 probabl
23	164.5	2.5	249	T41814	IAP2 orf71 - Bomby
24	159.5	2.4	249	H72858	apoptosis-inhibito
25	159.5	2.4	4845	T31067	BIR repeat contain
26	156	2.3	236	T10343	inhibitor of apopt
27	155.5	2.3	383	F96582	hypothetical prote
28	149.5	2.2	115	B96654	probable RING zinc
29	139	2.1	124	T01251	hypothetical prote
30	139	2.1	489	S15349	mdm2 protein - mou
31	136.5	2.0	960	S72284	DNA-directed RNA p
32	132.5	2.0	864	T01393	apoptosis-inhibito
33	130	1.9	428	T48167	hypothetical prote
34	124	1.9	960	S72284	DNA-directed RNA p
35	123.5	1.8	433	JC7678	RING finger protei
36	122.5	1.8	237	T52432	hypothetical prote
37	122.5	1.8	823	D86165	protein P15K9.3 [i
38	120	1.8	711	C84767	hypothetical prote
39	120	1.8	943	S68824	ring protein, cyto
40	119	1.8	269	T40371	probable zinc fing
41	119	1.8	491	S24354	p53-binding protei
42	117	1.8	714	C90100	hypothetical prote
43	117	1.8	731	A99106	hypothetical prote
44	116.5	1.7	870	G86450	F5D14.31 protein -
45	116.5	1.7	1019	E90097	hypothetical prote

ALIGNMENTS

RESULT 1  
A45679  
inhibitor-of-apoptosis polypeptide (IAP) - Cydia pomonella granulosis virus CpGV  
C:Species: Cydia pomonella granulosis virus CpGV  
C>Date: 21-Sep-1993 #sequence\_revision 25-Apr-1997 #text\_change 09-Jul-2004  
C/Accession: A45679  
C/Crook, N.E.; Clem, R.J.; Miller, L.K.  
J. Virol. 67, 2168-2174, 1993  
A:Title: An apoptosis-inhibiting baculovirus gene with a zinc finger-like motif.  
A:Reference number: A45679; MUID:9318168; PMID:8445726  
A:Accession: A45679  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-275 <CRO>  
A:Cross-references: UNIPROT:P41436; UNIPARC:UPI000012D0CE; GB:L05494; NID:9289583; PIDN:/  
C:Superfamily: viral apoptosis inhibitor IAP; RING finger homology

Alignment Scores:

Pred. No.: 2.94e-75  
Score: 966.00  
Percent Similarity: 72.66%  
Best Local Similarity: 59.17%  
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Gaps: 3

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QY	467	TTTTTGAGCGCGAACAATGGCCGACGAGATTCTACTACCGGTGCGGAGGA	526
DB	21	PheueSerProGluThrMetAlaLysAsnGlyPheTyTruGluYAspSerAspGlu	40
QY	527	GTCGTCTGCTCTTCTGTAGTAGTAATATGAGTGGGTCGAAGCGAGATCTCGCC	586

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Db      41 ValArgCysAlaPheCysValyValGluIleMetArgTrpIysGluIleProAla 60
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      61 AlaAspHisValyValTrpAlaProGlnCysProPheValy----- 74
      647 GCTGGGGAGAGGCGACCGCTGTCCGTAGAGCAATGTGGGCGCACTGGCGCCAGCAG 706
      75 -----GlyIleAspValCysGlySerIleValThrThrAsn 86
      707 -----CCTCCCGCATGCGCGCCCGGACGCGGACGCGGCTATCC 745
      87 AsnIleGlnAsnThrThrThrHisAspThrIleIleGlyProAlaHisProIyValA 106
      746 ACCGAGCGCGCGCGCTGCGCACCTTCAGAGACTGGCGAGACTATGCGCAAAACCC 805
      107 HisGluAlaAlaIArgValIysSerPheHisAsnTrpProArgCysMetIySGlnArgPro 126
      806 GAGGAACCTGGCAGAGCGCGGATTTCTTATACAGGCCAAGCTGACAAACGAATGCTTC 865
      127 GluGlnMetIleAspAlaGlyPhePheTrpGlyTrpGlyAspAsnThrIySypHe 146
      866 TATTGGACGAGGCGCTAAAGATTGGGAAAGGATGAGCTCCGTCGGAACAGCACGCC 925
      147 TyrCysAspGlyGlyLeuIyAspTrpGluProGluAspValProItrpGluGlnHisVal 166
      926 AGATGTTTCGACCGCTGCGCGCTGACGTGCAATGTGTGAAGAGACTGATCATTCAGAG 985
      167 ArgTrpPheAspArgCysAlaTrpValGlnGluValIySglYArgAspTrpValGlnIyS 186
      986 GTGAACTCGGAGGCGCACTGGCGATA-----TTCGCTAGCGAAGAAAGACGCCGCC 1036
      187 ValIleThrGluIleCysValIleuProGlyGluAsnThrValSerThrIleAlaPro 206
      1037 ACCAATGATTCGACTAAGAACGTCGCCCAAGAGGGGAGAAACATTGTGATGACTTAA 1096
      207 ValSerGluProIleProGluThrIySglIleGluIySgluProGlnIyGluAspSerIyS 226
      1097 ATATGTAAATATATTATTCCTCGAGAGCGTAAACGTGTGCTTCGTGCGCGTGGCCAGTG 1156
      227 LeuCysIySglIleCysTrpValGlnGluCysIleValCysPheValIProCysGlyHisVal 246
      1157 GTGGCGTGGCCCAAGTGGCGCTGTGCAAGCAAGTGGCCGATGTGTGCGCAGACGTTG 1216
      247 ValAlaCysAlaIySglCysAlaIeuserValAspIyCysPromeCysArgIySglIleVal 266
      1217 AGCAATGCGGTGGCGCTGACTTCTCG 1243
      267 ThrSerValLeuIyValIyTrpPheSer 275

```

**RESULT 2**  
 T10304  
 Inhibitor of apoptosis protein 3 - Oryzia pseudotenuata nuclear polyhedrosis virus  
 C/Species: Oryzia pseudotenuata nuclear polyhedrosis virus, OpMV  
 C/Date: 16-Jul-1999 #sequence\_revision 16-Jul-1999 #text\_change 15-Sep-2000  
 C/Accession: T10304  
 R/Authors, C.A.; Ruseell, R.R.; Funk, C.D.; Evans, J.; Harwood, S.; Rohmann, G.F.  
 Virology 229, 381-399, 1997  
 A/Title: The sequence of the Oryzia pseudotenuata multinnucleocapsid nuclear polyhedrosis  
 A/Reference number: Z17011; PMID:972171300; PMID:9126251  
 A/Accession: T10304  
 A/Status: preliminary; translated from GB/EMBL/DBJ  
 A/Molecule type: DNA  
 A/Residues: 1-268 <AHR>  
 A/Cross-references: UNIPARC:UPI000006180F, EMBL:U75930; NID:G2934903; PIDN:AAC59034.1; F  
 C/Superfamily: Viral apoptosis inhibitor IAP; RING finger homology  
 F:217-261/Domain: RING finger homology <RRN>

Alignment Scores:  
 Pared. No.: 2,986-66 Length: 268  
 Score: 862.00 Matches: 150  
 Percent Similarity: 65.82% Conservative: 31  
 Best Local Similarity: 54.55% Mismatches: 72

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Query Match: 12.88% Indels: 22
DB: 2 Gaps: 2
US-10-041-859a-1 (1-3773) x T10304 (1-268)
      413 GACATCGCTCGTAAGAGAGAGTCTGAAACATTTGATCAAGGCGCGTACGTTTGG 472
      14 AspMetIyAsnIyValAlaIArgLeuGlyThrTrpHisAsnTrpProValGlnPheLeu 33
      473 ACCCGGAACAAATTGACCGCGCAACGATTTCTACTACCTGCGTGCAGCAGAAAGTGC 532
      34 GluProSerArgMetIleAlaIserGlyPheTrpTrpLeuGlyArgGlyAspGluValArg 53
      533 TGTGCTTTGTGAAGTAGAAATTAATGAGTGGGTGAAAGCGAGCATCTGCGCGCAT 592
      54 CysAlaPheCysLeuValGluIleThrAsnTrpValArgIyAspAspProGluThrAsp 73
      593 CATCGAGATGGCGCGCGCGCGCGCTCCCTTTGTACGAAACAAATGTATACCAACGCTGG 652
      74 HisIyArgTrpAlaProGlnCysProPheValArgAsnAsnAlaHisAspThrProHis 93
      653 GGAGAGCGACACGCTGTCCGTAGAGACGAATGTGGGCGCAGTGCAGCGACCTCC 712
      94 AspArgAla-----ProPro 98
      713 CGCATGCCGCGCGCGCGTGCACGCGCGTACTCCACGAGCGCGCGGCTGCCACCTTC 772
      99 AlaArgSerAlaAlaAlaHisProGlnTrpAlaThrGluAlaAlaIArgLeuArgThrPhe 118
      773 AAGGACTGGCGCGAGAGCTATGCGCGCAAAACCGAGAGAACTGGCAGAGCGCGATCTTC 832
      119 AlaGluTrpProArgGlyLeuIySglIyAspArgProGluGluIleAlaGlyPhePhe 138
      833 TATACAGCGCAAGTAGTACAAACGAATGCTTCTATTCGACGAGAGGCTTAAAGATTG 892
      139 TyrThrGlyGlnIyAspIySglThrArgCysPheCysAspGlyGlyLeuIyAspTrp 158
      893 GAAAGCGATGACGTTCCGTGGGAAACAGACGCCAGATGGTTCGACCGTGGCGTACGTG 952
      159 GluProAspAspAlaProItrpGlnGlnHisAlaIArgTrpIyAspArgCysGluTrpVal 178
      953 CAATTGTGAAGAGAGCTGACTACATTCAGAAAGTGAAGTGGAGGCGCACTGCGATATCT 1012
      179 LeuIleValIyGlyIyArgAspPheValGlnArgValMetThrGluIleCysValIyArg 198
      1013 GCTAGCGAAGAAAGAACAGCGCGCGCACCAATGATTCGACTAAGAACGTCGCCCAAGAGGCG 1072
      199 AspAlaAspAsnGluProHisIleGluIyArgProAlaVal----- 211
      1073 GAGAAACATTTGGATGACTCTAATAATATGTAATATGTTATTCGAGAGCGTAACTG 1132
      212 GluAlaGluValAlaIAspAspArgLeuCysIySglIleCysLeuGlyIyAlaGluIySerVal 231
      1133 TGTGTTGTGCGCGTGGCGCGCACGTTGCGTGGCGCGCAAGTGGCGCTGTGACAGCAAG 1192
      232 CysPheValIProCysGlyIyHisValIyAlaIyCysGlyIyCysAlaIyAlaGlyValThrThr 251
      1193 TGGCGATGTGTGCGCAGAGCGTTTCAAGATGGGCGTGGCGCTCTAC 1237
      252 CysProValCysArgGlyGlnLeuAspIyValAlaValArgMetCysTrp 266

```

**RESULT 3**  
 A53989  
 apoptosis-inhibiting protein - Oryzia pseudotenuata multicapsid nuclear polyhedrosis viru  
 C/Species: Oryzia pseudotenuata multicapsid nuclear polyhedrosis virus, OpMV  
 C/Date: 15-Oct-1994 #sequence\_revision 15-Oct-1994 #text\_change 09-Jul-2004  
 C/Accession: A53989  
 R/Birnbaum, M.J.; Clem, R.J.; Miller, L.K.  
 J. Virol. 68, 2521-2528, 1994  
 A/Title: An apoptosis-inhibiting gene from a nuclear polyhedrosis virus encoding a polype  
 A/Reference number: A53989; PMID:94187094; PMID:8139034  
 A/Accession: A53989  
 A/Status: preliminary

GenCore version 5.1.6  
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OM nucleic - protein search, using frame\_plus\_n2p model

Run on: November 26, 2005, 10:20:33 / Search time 289.5 Seconds  
(without alignments)  
11452.685 Million cell updates/sec

Title: US-10-041-859A-1  
Perfect score: 6692  
Sequence: 1 cattataaccacttcac.....tgcgctcctactctcgtga 3773

Scoring table: BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 2443163 seqs, 439378781 residues  
Total number of hits satisfying chosen parameters: 4886326

Minimum DB seq length: 0  
Maximum DB seq length: 200000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:  
-MODE=frame+ n2p.model -DEV=xlh  
-Q=cm2.1/USPTO.spool/US10041859/runat.23112005.100311.11846/app.query.fasta.1.3911  
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-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45  
-DOCALIGN=200 -THR SCORE=pcr -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL  
-OUTPRT=pco -NOR=exc -HEA=SIZE=500 -MINLEN=0 -MAXLEN=2000000000  
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Database : A\_Geneseq\_21: \*  
1: geneseqp1980s: \*  
2: geneseqp1990s: \*  
3: geneseqp2000s: \*  
4: geneseqp2001s: \*  
5: geneseqp2002s: \*  
6: geneseqp2003as: \*  
7: geneseqp2003bs: \*  
8: geneseqp2004s: \*  
9: geneseqp2005s: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1887	28.2	346	5	ABB78046
2	1319	19.7	377	4	AAE07881
3	767.5	11.5	263	5	ABB09488
4	721.5	10.8	438	4	ABB48189
5	719.5	10.8	438	4	ABB61858
6	719.5	10.8	438	4	ABB67347
7	719.5	10.8	438	4	ABB48188
8	719.5	10.8	438	4	ABB48190
9	719.5	10.8	438	8	ADO08093

10	713.5	10.7	438	4	ABB48192	Abb48192 Drosophila
11	713.5	10.7	438	4	AAAB48191	Abb48191 Drosophila
12	711.5	10.6	438	4	AAAB48196	Abb48196 Drosophila
13	709.5	10.6	438	4	AAAB48197	Abb48197 Drosophila
14	708.5	10.6	438	4	AAAB48193	Abb48193 Drosophila
15	708.5	10.6	438	4	AAAB48194	Abb48194 Drosophila
16	576.5	8.6	434	4	AAAB48195	Abb48195 Drosophila
17	526.5	7.9	604	2	AAAW19747	AAW19747 Human inh
18	526.5	7.9	604	2	AAAW13546	AAW13546 Human c-I
19	526.5	7.9	604	2	AAAY52703	AAy52703 Human cel
20	526.5	7.9	604	2	AAAY33997	AAy33997 Human cel
21	526.5	7.9	604	6	ABU07431	ABu07431 Protein d
22	526.5	7.9	604	6	ABU07431	ABu07431 Protein d
23	526.5	7.9	604	7	ADBB80948	ADb80948 RING-SH c
24	526.5	7.9	604	7	AAAB39811	AAe39811 Human cel
25	526.5	7.9	604	8	ADG87135	Adg87135 Human CIA
26	526.5	7.9	604	8	ADH74643	Adh74643 Human CIA
27	526.5	7.9	604	8	ADSR8171	AdSR8171 Human pro
28	526.5	7.9	604	8	ADRR89114	Adr89114 Human IAP
29	526.5	7.9	604	8	ADRR89114	Adr89114 Human IAP
30	526.5	7.9	604	8	ADU22899	Adu22899 Human bla
31	525.5	7.9	600	2	AAAG92298	AAe92298 Murine HI
32	525.5	7.9	600	6	ABP72155	ABp72155 Mouse inh
33	524.5	7.8	604	2	AAAW19582	AAw19582 Human apo
34	524.5	7.8	604	2	AAAG69295	AAg69295 Human HIA
35	524.5	7.8	604	5	ABG65664	ABg65664 Human inh
36	517.5	7.7	602	5	ABG65667	ABg65667 Mouse inh
37	516.5	7.7	602	2	AAW19585	AAw19585 Mouse apo
38	507.5	7.6	618	2	AAW19583	AAw19583 Human apo
39	507.5	7.6	618	2	AAW69296	AAw69296 Human HIA
40	507.5	7.6	618	5	ABG65665	ABg65665 Human inh
41	501	7.5	497	7	AD139803	Ad139803 Drosophila
42	500.5	7.5	486	2	AAW19745	AAw19745 Mouse inh
43	500.5	7.5	618	2	AAW19746	AAw19746 Human inh
44	500.5	7.5	618	2	AAW13545	AAw13545 Human c-I
45	500.5	7.5	618	2	AAAY33998	AAy33998 Human cel

## ALIGNMENTS

RESULT 1	ABB78046	standard; protein; 346 AA.
ID	ABB78046	
XX	XX	
AC	ABB78046;	
XX	XX	
DT	22-OCT-2002	(first entry)
XX	XX	
DE	XX	Amino acid sequence of inhibitor of apoptosis protein Bmi1P.
XX	XX	
KW	XX	Inhibitor of apoptosis protein; IAP; Bmi1P; silkworm; apoptosis; insect;
KW	XX	Spodoptera frugiperda; Insult-resistant plant; caspase.
XX	XX	
OS	XX	Bombix mori.
XX	XX	
FT	XX	Location/Qualifiers
FT	Domain	74..140
FT	Domain	/note="BIR domain 1"
FT	Domain	182..249
FT	Domain	/note="BIR domain 2"
FT	Domain	298..314
FT	Domain	/note="RING domain"
XX	XX	
PN	XX	W0200253586-A2.
XX	XX	
PD	XX	11-JUL-2002.
XX	XX	
PF	XX	07-JAN-2002; 2002W0-US000314.
XX	XX	
PR	XX	08-JAN-2001; 2001US-0260478P.
XX	XX	
PA	XX	(BURN-) BURNHAM INST.
XX	XX	

PI Maeda S, Huang Q, Reed JC, Devereaux QL;  
 XX WPI; 2002-590628/63.  
 DR N-PSDB; ABQ78228.  
 XX  
 PT Novel recombinant polypeptide, inhibitor of apoptosis protein family  
 member BmiAP from silkworm Bombyx mori BmN cells, useful for inhibiting  
 apoptosis and identifying an agent that modulates activity of  
 PT polypeptide.  
 XX  
 PS Claim 39; Page 31; 62pp; English.  
 XX  
 CC The present score represents a polypeptide which is an inhibitor of  
 CC apoptosis protein (IAP) family member, and designated BmiAP. BmiAP is  
 CC derived from silkworm Bombyx mori BmN cells. The BmiAP polypeptide  
 CC contains two baculoviral IAP repeat (BIR) domains, followed by a RING  
 CC domain. BmiAP polypeptides and polymuclotides are useful for inhibiting  
 CC apoptosis in insect cells, especially Spodoptera frugiperda or Bombyx  
 CC mori cells, and mammalian cells, and plant cells. They are also useful  
 CC for generating a biotic or abiotic insect-resistant plant. BmiAP is also  
 CC useful for inhibiting caspases

SO Sequence 346 AA;

Alignment Scores:

Pred. No.: 3.32e-182 Length: 346  
 Score: 1887.00 Matches: 346  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 28.20% Indels: 0  
 DB: Gaps: 0

US-10-041-859A-1 (1-3773) x ABB78046 (1-346)

QY 206 ATGGAGTTGACGAAAGTTGGTAAATATGAGCTGCCGCGACGTTGGATGTTAAAT 265  
 DB 1 MetGluLeuThrValAlaValAsnGlyAlaAlaThrLeuValMetLeuValAsn 20  
 QY 266 GCGCGGAGATGCAAAATGCGACCTTTCATTGTCCTCGCTCATGTTATCTCGTGAAGTCT 325  
 DB 21 AlaArgAspAlaValMetArgProPheIleGlyProLeuMetLeuSerSerCysGluSer 40  
 QY 326 TCACGACATCCACTCCCGTCACTTGTGTCGTCAGCTGATTAACGATTAATCAGAC 385  
 DB 41 SerThrThrSerThrLeuProSerProSerSerSerAlaAspValThrAspAsnHisAsp 60  
 QY 386 ACATTGCACTTCTTCTGATATGCCCGGACATGCGTCGTGAAGGAAAGCTCGAAATCA 445  
 DB 61 ThrPheAsnPheLeuProAspMetProAspMetArgArgGluGluValArgLeuValThr 80  
 QY 446 TTTCATCAGTGGCCGCTTACGTTTGTGACCGCGGAAATTTGGCCCGCAACGAGATTCTAC 505  
 DB 81 PheAspGlnTrpProValThrPheLeuThrProGluGlnLeuAlaArgAsnGlyPheThr 100  
 QY 506 TACCTCGTGGCGGCGACGAAAGTGCTGTCTTTCTGTAAGGTAGAAATTAAGAGTGG 565  
 DB 101 TyrLeuGlyArgGlyValAspGluValCysCysAlaPheCysValGluIleMetArgTrp 120  
 QY 566 GTTCGAGGCGGACGATCTCGCCCGGATCATCGAGATGGCGCCGACAGTGTCCCTTTGTA 625  
 DB 121 ValGluGlyAspAspProAlaAlaAspHisArgArgTrpAlaProGlnCysProPheVal 140  
 QY 626 CGAAACAATATGATATCCCAAGCTGGGGGAGAGGCGACCGCTTCGTTAGAGACGAATGT 685  
 DB 141 ArgGlyGlnMetCysTrpAlaAsnAlaGlyGlyGluAlaThrAlaValGlyArgAspGluCys 160  
 QY 686 GGGGCGGATGGCGGCGACGACGCTCCCGCATGCCCGGCGCCGCGTACCGCGGTAATCC 745  
 DB 161 GlyAlaSerAlaAlaThrGlnProProArgMetProGlyProValHisAlaArgTyrSer 180  
 QY 746 ACCGAGGCGCGCGGCTCGGACATTCAGAGACTGGCCGAGAGATGATGCCCAAAATCC 805  
 DB 181 ThrGluAlaAlaArgLeuAlaThrPheLeuValAspTrpProArgArgMetArgGlnValPro 200

QY 806 GAGAACTGGCAGAGCGCGGATTTCTTATACAGGCCAAAGTGACAAAGAAATGCTTC 865  
 DB 201 GluGluLeuAlaGluAlaValPhePheThrGlyGlnGlyAspValThrValCysPhe 220  
 QY 866 TATTGCGACGAGGCGCTTAAAGATTGGAAAGCGATGACGTTCCGTGGAAACAGACGCC 925  
 DB 221 TyrCysAspGlyGlyLeuValAspTrpGluSerAspAspValProTrpGluGlnHisAla 240  
 QY 926 AGATGGTTGACCGCGCGGTACGTCGAATTTGGTAAAGGACGTCATCATTCGAAG 985  
 DB 241 ArgTrpPheAspArgCysAlaTrpValGlnLeuValValGlyAlaArgAspTrpTyrIleGln 260  
 QY 986 GTGAATCGGAGCGCAGTCGATATCTGTAGCGAAGAAAGACAGCGCCCAATGAT 1045  
 DB 261 ValIleSerGluAlaThrAlaIleSerAlaSerAlaSerGluGluGlnAlaAlaThrAsnAsp 280  
 QY 1046 TCAGCTAAGACGTCGCCCAAGAGGCGGAGAAACATTGGATGACTCTTAAATATGTTAA 1105  
 DB 281 SerThrValAsnValAlaGlnGlnGlyGlyValIleLeuAspAspSerTyrIleCysVal 300  
 QY 1106 ATATGTTATTCGAGAGGAGTAAAGTCGTGTCGTCGCGGCGGCGACGTCGTGGGTCG 1165  
 DB 301 IleCysTyrSerGluGluArgAsnValCysPheValProCysGlyHisValAlaAlaCys 320  
 QY 1166 GCCAAGTGGCGCGCTGTGCAAGCAAGTCCCGATGTGTGCGACGTTTCAAGAAATGCG 1225  
 DB 321 AlaValCysAlaLeuSerThrAspValCysProMetCysArgArgThrAsnHisAla 340  
 QY 1226 GTGCGGCTTACTTCTCG 1243  
 DB 341 ValArgLeuTyrPheSer 346

RESULT 2  
 AAE07881  
 ID AAE07881 standard; protein; 377 AA.  
 XX  
 AC AAE07881;  
 XX  
 DT 01-NOV-2001 (first entry)  
 XX  
 DE Fall armyworm inhibitor of apoptosis (IAP) protein.  
 XX  
 KW Fall armyworm; inhibitor of apoptosis; IAP; transgenic plant;  
 KW apoptosis inhibitor; therapy; acquired immune deficiency syndrome; AIDS;  
 KW neurodegenerative disease; Alzheimer's disease; aplastic anaemia;  
 KW Parkinson's disease; amyotrophic lateral sclerosis; retinitis pigmentosa;  
 KW myelodysplastic syndrome; toxin-induced liver disease; ischaemic injury;  
 KW myocardial infarction; stroke; reperfusion injury; cancer; neotropic;  
 KW autoimmune disorder; lupus erythematosus; multiple sclerosis; vasotropic;  
 KW insecticide; viral infection; anti-HIV; human immunodeficiency virus;  
 KW neuroprotective; antianemic; cardiac; cerebroprotective; vulnerary;  
 KW cyrostatic; immunosuppressive; virucide; antialcoholic.  
 XX  
 OS Spodoptera frugiperda.  
 OS  
 PN MO200159108-A2.  
 PN  
 PD 16-AUG-2001.  
 PD  
 PF 07-FEB-2001; 2001WO-US004071.  
 PF  
 PR 10-FEB-2000; 2000US-00502528.  
 PR  
 PA (REGC ) UNIV CALIFORNIA.  
 PA (MAED/) MAEDA H.  
 PA  
 PI Maeda S, Hammock BD, Huang Q, Maeda H;  
 PI WPI; 2001-514667/56.  
 DR N-PSDB; AAD14419.  
 DR  
 XX Novel nucleic acid construct comprising cDNA encoding inhibitor of

GenCore version 5.1.6  
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OM nucleic - nucleic search, using bw model

Run on: November 26, 2005, 10:10:03 ; Search time 224 Seconds  
(without alignments)  
2503.116 Million cell updates/sec

Title: US-10-041-859A-1  
Perfect score: 3773  
Sequence: 1 catctaaactcactctcac.....tgcgcctcactctcgtga 3773

Scoring table: IDENTITY\_NUC  
Gapop 10\_0, Gapext 1.0

Searched: 3205263 seqs, 74304013 residues  
Total number of hits satisfying chosen parameters: 6410526

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications NA New:  
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2: /cgn2\_6/ptodaca/2/pubpna/US06\_NEW\_PUB.seq:\*  
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5: /cgn2\_6/ptodaca/2/pubpna/US09\_NEW\_PUB.seq:\*  
6: /cgn2\_6/ptodaca/2/pubpna/PCr\_NEW\_PUB.seq:\*  
7: /cgn2\_6/ptodaca/2/pubpna/US11\_NEW\_PUB.seq:\*  
8: /cgn2\_6/ptodaca/2/pubpna/US11\_NEW\_PUB.seq3:\*  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	91.8	2.4	1068	US-11-135-855-21	Sequence 21, Appl
2	81	2.1	769	US-11-135-855-22	Sequence 22, Appl
3	47.4	1.3	3159	US-10-793-626-4112	Sequence 4112, Ap
4	47.4	1.3	3376	US-10-793-626-4055	Sequence 4055, Ap
5	46.2	1.2	4248	US-10-793-626-3669	Sequence 3669, Ap
6	45.2	1.2	3073	US-10-793-626-3606	Sequence 3606, Ap
7	42.6	1.1	3549	US-10-793-626-4022	Sequence 4022, Ap
8	42.2	1.1	1314	US-11-074-176-151	Sequence 151, App
9	42.2	1.1	3478	US-10-793-626-3605	Sequence 3605, Ap
10	41	1.1	3165	US-10-793-626-3360	Sequence 3360, Ap
11	40.8	1.1	1299	US-10-793-626-779	Sequence 779, App
12	40.8	1.1	3119	US-10-793-626-4270	Sequence 4270, Ap
13	40.8	1.1	3393	US-10-793-626-4010	Sequence 4010, Ap
14	40.8	1.1	3645	US-10-793-626-4110	Sequence 4110, Ap
15	40.8	1.1	4017	US-10-793-626-4104	Sequence 4104, Ap
16	40.6	1.1	3458	US-10-793-626-3510	Sequence 3510, Ap
17	40.2	1.1	3189	US-10-793-626-3694	Sequence 3694, Ap
18	40.2	1.1	340000	US-11-102-978-3	Sequence 3, Appl
19	40	1.1	1644	US-11-077-550-23	Sequence 23, Appl
20	40	1.1	2097	US-10-793-626-2387	Sequence 2387, Ap
21	40	1.1	2574	US-11-077-550-21	Sequence 21, Appl
22	40	1.1	2574	US-11-077-550-27	Sequence 27, Appl
23	40	1.1	3028	US-10-793-626-4247	Sequence 4247, Ap

C	24	40	1.1	3337	1	US-10-793-626-3655	Sequence 3655, Ap
C	25	40	1.1	3350	1	US-10-793-626-4018	Sequence 4018, Ap
C	26	40	1.1	3509	9	US-11-077-550-19	Sequence 19, Appl
C	27	39.8	1.1	2902	1	US-10-793-626-4170	Sequence 4170, Ap
C	28	39.8	1.1	3617	1	US-10-131-826A-409	Sequence 409, Appl
C	29	39.4	1.0	3111	1	US-10-793-626-4268	Sequence 4268, Ap
C	30	39.4	1.0	3127	1	US-10-793-626-3575	Sequence 3575, Ap
C	31	39.4	1.0	3927	1	US-10-793-626-4223	Sequence 4223, Ap
C	32	39.4	1.0	3961	1	US-10-793-626-3597	Sequence 3597, Ap
C	33	39.4	1.0	4094	1	US-10-793-626-3641	Sequence 3641, Ap
C	34	39.4	1.0	4189	1	US-10-793-626-3898	Sequence 3898, Ap
C	35	39.4	1.0	4248	1	US-10-793-626-3669	Sequence 3669, Ap
C	36	39.2	1.0	3506	1	US-10-793-626-3423	Sequence 3423, Ap
C	37	39	1.0	2476	1	US-10-131-826A-489	Sequence 489, Appl
C	38	39	1.0	3462	1	US-10-793-626-4440	Sequence 4440, Ap
C	39	39	1.0	3536	1	US-10-793-626-4139	Sequence 4139, Ap
C	40	39	1.0	3939	1	US-10-793-626-3938	Sequence 3938, Ap
C	41	38.8	1.0	2683	1	US-10-793-626-3709	Sequence 3709, Ap
C	42	38.8	1.0	3008	1	US-10-793-626-3513	Sequence 3513, Ap
C	43	38.8	1.0	3037	1	US-10-793-626-3901	Sequence 3901, Ap
C	44	38.8	1.0	3073	1	US-10-793-626-3606	Sequence 3606, Ap
C	45	38.8	1.0	3116	1	US-10-793-626-4248	Sequence 4248, Ap

ALIGNMENTS

RESULT 1  
US-11-135-855-21  
Sequence 21, Application US/11135855  
Publication No. US20050255557A1  
GENERAL INFORMATION:  
APPLICANT: SMITHKLINE BEECHAM CORPORATION  
APPLICANT: SMITHKLINE BEECHAM P.I.C.  
TITLE OF INVENTION: NOVEL COMPOUNDS  
FILE REFERENCE: GP50013  
CURRENT APPLICATION NUMBER: US/11/135,855  
CURRENT FILING DATE: 2005-05-24  
PRIOR APPLICATION NUMBER: US/10/203,708  
PRIOR FILING DATE: 2002-08-13  
PRIOR APPLICATION NUMBER: PCT/US01/04703  
PRIOR FILING DATE: 2001-02-14  
PRIOR APPLICATION NUMBER: 60/182,172  
PRIOR FILING DATE: 2000-02-14  
PRIOR APPLICATION NUMBER: 60/186,084  
PRIOR FILING DATE: 2000-02-29  
NUMBER OF SEQ ID NOS: 46  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 21  
LENGTH: 1068  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-11-135-855-21  
Query Match 2.4%; Score 91.8; DB 7; Length 1068;  
Best Local Similarity 60.7%; Pred. No. 1.2e-10;  
Matches 150; Conservative 0; Mismatches 97; Indels 0; Gaps 0;  
Db 745 CACCGAGCGCGCGCTGCCACCTTCAAGACGTGCGGACGATGCGCCAAAACC 804  
255 CTCGAGGAGATTGCGTCTGCTCTCTCTATGACGTGCGCGCTGACGTGAGGTCAC 314  
Qy CGAGCACTGCGAGAGCGCGATTTCTTATACAGGCCAAGTGACAAAAGTCTT 864  
315 CGAGCTGCTGCGCTGCTGCGCGCTTCTTCCACAGGCGCATCAGAGCAAGGTGAGTCTT 374  
Qy CTAATGCGACGAGGCGCTAAAGATTGGGAAACGATGACGTTCCGTGGGAACGACGCG 924  
865 CTAATGCGACGAGGCGCTAAAGATTGGGAAACGATGACGTTCCGTGGGAACGACGCG 924  
Db CTCTCTGTAAGGGGCGCTGAGAGCTGGAAGCGCGGAGACGACCTCTGACGAGCATGC 434  
375 CTCTCTGTAAGGGGCGCTGAGAGCTGGAAGCGCGGAGACGACCTCTGACGAGCATGC 434  
Qy CAGATGTTGACCGCTGCGCGTACGTGCAATTGTAAGGAGCGTACCTACTTACGAA 984  
925 CAGATGTTGACCGCTGCGCGTACGTGCAATTGTAAGGAGCGTACCTACTTACGAA 984  
Db CAAGTGGTCCCGAGCTGTGCTGCTCGCTCGGTCAAAAGAAAGACTTTTCCACAG 494  
435 CAAGTGGTCCCGAGCTGTGCTGCTCGCTCGGTCAAAAGAAAGACTTTTCCACAG 494

OY 985 GGTGAAG 991  
|||  
Db 495 TGTGAG 501

RESULT 2  
US-11-135-855-22  
; Sequence 22, Application US/11135855  
; Publication No. US2005025557A1  
; GENERAL INFORMATION:  
; APPLICANT: SMITHKLINE BEECHAM CORPORATION  
; APPLICANT: SMITHKLINE BEECHAM P.L.C.  
; TITLE OF INVENTION: NOVEL COMPOUNDS  
; FILE REFERENCE: GP50013  
; CURRENT APPLICATION NUMBER: US/11/135,855  
; PRIOR FILING DATE: 2005-05-24  
; PRIOR APPLICATION NUMBER: US/10/203,708  
; PRIOR FILING DATE: 2002-08-13  
; PRIOR APPLICATION NUMBER: PCT/US01/04703  
; PRIOR FILING DATE: 2001-02-14  
; PRIOR APPLICATION NUMBER: 60/182,172  
; PRIOR FILING DATE: 2000-02-14  
; PRIOR APPLICATION NUMBER: 60/186,084  
; NUMBER OF SEQ ID NOS: 46  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 22  
; LENGTH: 769  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-11-135-855-22

Query Match 2.1%; Score 81; DB 7; Length 769;  
Best Local Similarity 60.7%; Pred. No. 1.9e-08;  
Matches 150; Conservative 0; Mismatches 95; Indels 2; Gaps 1;

OY 745 CACCGAGCCGCGCGCTCCGCACTTCAAGAGCTGCGCCAGACGTATGCGCCAAAACC 804  
|||  
Db 255 CTGTGAGAGATTGCTGTGCGCTCTCTTCTATGACTGCGCGCTGACGTGAGGCGCAC 314  
|||  
OY 805 CGAGGAACTGCGAGAGCGCGGATTTCTTATPACAGCCCAAGTGAACAAAGAAATGCTT 864  
|||  
Db 315 CGAGCTGCTGCTGCTGCTGCTGCTCTTCCACACAGGCGCATCAGAACAAAGGTGAGTCTT 374  
|||  
OY 865 CTATTTGAGAGGAGGCTTAAGATTGGGAAGGATGATGATTCCTGCGGAACAGCACGC 924  
|||  
Db 375 CTCTGCTATGGGGGCTGCAAGCTGGAAGCGGGGAGAGACCCCTGGACGAGCATGC 434  
|||  
OY 925 CAGATGTTGACCGCTGCGCGTACGTGCAATTGTTGAAGAGCGTACTACATTTCAGAA 984  
|||  
Db 435 CAAGTGGTTC--CCCTGTGAGTTCCTGCTCCGCTCAAAAGAAAGACATTGTCCACAG 492  
|||  
OY 985 GGTGAAG 991  
|||  
Db 493 TGTGAG 499

RESULT 3  
US-10-793-626-4112/c  
; Sequence 4112, Application US/10793626  
; Publication No. US20050255478A1  
; GENERAL INFORMATION:  
; APPLICANT: KIMMERLY, WILLIAM JOHN  
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS  
; FILE REFERENCE: PU3480US  
; CURRENT APPLICATION NUMBER: US/10/793,626  
; PRIOR FILING DATE: 2004-03-04  
; PRIOR APPLICATION NUMBER: 60/164,258  
; PRIOR FILING DATE: 1999-11-09  
; NUMBER OF SEQ ID NOS: 4472  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 4112

; LENGTH: 3159  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: synthetic  
US-10-793-626-4112

Query Match 1.3%; Score 47.4; DB 1; Length 3159;  
Best Local Similarity 45.3%; Pred. No. 0.42;  
Matches 216; Conservative 0; Mismatches 256; Indels 5; Gaps 1;

OY 1854 TAATGATTCAGAAATTATTAATGACTATATTTGCTCTGTAATTAATATATATA 1913  
|||  
Db 2271 TATTTATATACATATTCATTTCTTAATTTTACAAATCTTTATTTGCTTCTTCAATAT 2212  
|||  
OY 1914 TACTATTTATGATTAATTCGACATTAATTTGCAATTCGCTAAGATACAAATCAATA 1973  
|||  
Db 2211 CATTTTACATTAAGAACTTATATCATATTTAGAACAAATTTTAACTGAAATTAATAAT 2152  
|||  
OY 1974 CTATTTCACTGTAACCTCACTCAAAATAGTGAATGTGTGATTAATTAATGTTAAAT 2033  
|||  
Db 2151 TGACTTAATCGTTATTCATTTTATATATTCATTCATCCATGATATATGTTCTTTTAATTT 2092  
|||  
OY 2034 GTCTAATTTATTAATTAATGAGCAAGTTCATTTAATGTAATGTAATTAATTTATTT 2093  
|||  
Db 2091 CTGTAAATTTTGAATAATTTGTAATATATGAAACATAT-TCATACATATCTAGTT 2037  
|||  
OY 2094 TTACAAACATTTAATGATTAATCTGCTGCTGATTTTAAATGATACAGAAATTAACCCA 2153  
|||  
Db 2036 TCAATTTTCCATATCTATTAATGATTAATGCTGTTTAAATATTAATATATATATGA 1977  
|||  
OY 2154 ACACCTTAATGAAAGTTTATACATTTGCTGATTAATAAAATATCATATCAATTAATTA 2213  
|||  
Db 1976 ACAAGCAATGTAAGGCTTATTTATTAATAAAATATATTTCTTTATGATTAATTA 1917  
|||  
OY 2214 CAATGATTTTATTAATTTGTCAGAAACCAACATTTTGTAGACCTCGCTTTAGC 2273  
|||  
Db 1916 AATTAATTAAGAGATTAAGTATGCTTAATTTATTTATTTATTAATTTTAACTGAAACGGGTGG 1857  
|||  
OY 2274 AAGTATGATGACAAACCAATGTTGCTGATTCATTAATTTAGTTGTAACCAATAT 2330  
|||  
Db 1856 ATTAATTAATTTTACTGCAATATATACTCATGAATTAATTAATTTTAAACAAATGAT 1800  
|||

RESULT 4  
US-10-793-626-4055/c  
; Sequence 4055, Application US/10793626  
; Publication No. US20050255478A1  
; GENERAL INFORMATION:  
; APPLICANT: KIMMERLY, WILLIAM JOHN  
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS  
; FILE REFERENCE: PU3480US  
; CURRENT APPLICATION NUMBER: US/10/793,626  
; PRIOR FILING DATE: 2004-03-04  
; PRIOR APPLICATION NUMBER: 60/164,258  
; PRIOR FILING DATE: 1999-11-09  
; NUMBER OF SEQ ID NOS: 4472  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 4055  
; LENGTH: 3376  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: synthetic  
US-10-793-626-4055

Query Match 1.3%; Score 47.4; DB 1; Length 3376;  
Best Local Similarity 44.9%; Pred. No. 0.43;  
Matches 260; Conservative 0; Mismatches 316; Indels 3; Gaps 2;

OY 1770 ATTCTAATGAATCCAGATTTAAATGCTCATTAATTAATATAGAAACAGTTTAC 1829



QY 241 CGCACGTTGGTATGTTAAAAATGCGCGGATGCAAAAATGCGACTTTCAATTGGTCC 300  
DB 241 CGCACGTTGGTATGTTAAAAATGCGCGGATGCAAAAATGCGACTTTCAATTGGTCC 300  
QY 301 GCTCATGTTATCCTCGGTGAGTCTTCAACGACATCCACACTCCCGTCACTTCTGTCTC 360  
DB 301 GCTCATGTTATCCTCGGTGAGTCTTCAACGACATCCACACTCCCGTCACTTCTGTCTC 360  
QY 361 AGCTGTAATAACGGAATATACGACACATTCATCTTCTCTGATATGCGCAGATCGC 420  
DB 361 AGCTGTAATAACGGAATATACGACACATTCATCTTCTCTGATATGCGCAGATCGC 420  
QY 421 TCGTGAAGAGAAAGTCTGAAAAATTGATCAGTGGCCCGTTACGTTTTTGAACGCCGA 480  
DB 421 TCGTGAAGAGAAAGTCTGAAAAATTGATCAGTGGCCCGTTACGTTTTTGAACGCCGA 480  
QY 481 ACAATTGGCCCGGACGGAATTCATACCTCCGATCCGGGGGAGAAAGTGTGCTGTCTT 540  
DB 481 ACAATTGGCCCGGACGGAATTCATACCTCCGATCCGGGGGAGAAAGTGTGCTGTCTT 540  
QY 541 CTGTAAAGTGAATTAATGAGTGGGTGAAAGCGACGATCTGCGCGCATCATCGGAG 600  
DB 541 CTGTAAAGTGAATTAATGAGTGGGTGAAAGCGACGATCTGCGCGCATCATCGGAG 600  
QY 601 ATGGGCGCCCGACAGTCTCTTTGTACGAAAACAAAATGTATGCCAAACGCTGGGGAGAGGC 660  
DB 601 ATGGGCGCCCGACAGTCTCTTTGTACGAAAACAAAATGTATGCCAAACGCTGGGGAGAGGC 660  
QY 661 GACCGCTGTGCGTATGAGACGAATGTGGGGGCGATGTGGGCGCAACGACGCTCCCGCATGCC 720  
DB 661 GACCGCTGTGCGTATGAGACGAATGTGGGGGCGATGTGGGCGCAACGACGCTCCCGCATGCC 720  
QY 721 CGGCCCCGTGCAAGCGCGGTACTCAACGAGCGCGCGCTGCGCACTTCAAGGACTG 780  
DB 721 CGGCCCCGTGCAAGCGCGGTACTCAACGAGCGCGCGCTGCGCACTTCAAGGACTG 780  
QY 781 GCCGAGACGTATCGCCAAAAAATGCTTATGCGACGAGGGGCTAAAAATGGGAAAAAGCGA 840  
DB 781 GCCGAGACGTATCGCCAAAAAATGCTTATGCGACGAGGGGCTAAAAATGGGAAAAAGCGA 840  
QY 841 CCAAGGTGACAAAACGAAATGCTTATGCGACGAGGGGCTAAAAATGGGAAAAAGCGA 900  
DB 841 CCAAGGTGACAAAACGAAATGCTTATGCGACGAGGGGCTAAAAATGGGAAAAAGCGA 900  
QY 901 TGAAGTTCCTGTGGGAAACAGACCGCCAGATGTTCGACCGCTGCGCGTACGTTGCTTGGT 960  
DB 901 TGAAGTTCCTGTGGGAAACAGACCGCCAGATGTTCGACCGCTGCGCGTACGTTGCTTGGT 960  
QY 961 GAAAGGACGTGACTACATTCAAGAGTGAAGTGGAGGCGCATGCGATATCTGACGCA 1020  
DB 961 GAAAGGACGTGACTACATTCAAGAGTGAAGTGGAGGCGCATGCGATATCTGACGCA 1020  
QY 1021 AGAAGGAAACGAGCGCGCAACCAATTCGACTAAGAAAGTGGCCCAAGAGGCGCAAGAAAC 1080  
DB 1021 AGAAGGAAACGAGCGCGCAACCAATTCGACTAAGAAAGTGGCCCAAGAGGCGCAAGAAAC 1080  
QY 1081 TTTGATGACTCTAAAAATATGTAATATGTATTTCCGAGAGAGCTTAACTGTGCTTGGT 1140  
DB 1081 TTTGATGACTCTAAAAATATGTAATATGTATTTCCGAGAGAGCTTAACTGTGCTTGGT 1140  
QY 1141 GCCGTGCGGCAAGTGTGGCGGTGCGCAAGTGCAGCTGTGCAACGGAACAAGTGCAGAT 1200  
DB 1141 GCCGTGCGGCAAGTGTGGCGGTGCGCAAGTGCAGCTGTGCAACGGAACAAGTGCAGAT 1200  
QY 1201 GTGTGCAAGAGCTTACCAAGAAAGCGGTGCGCTCTACTTCTGTGAAAGAGACCTTCTCTG 1260  
DB 1201 GTGTGCAAGAGCTTACCAAGAAAGCGGTGCGCTCTACTTCTGTGAAAGAGACCTTCTCTG 1260  
QY 1261 CGAGCTGTATCTAATCACTTCAACCGGGCGGCTCTGAGGCTGTCTGAACCAACCTTTCGA 1320  
DB 1261 CGAGCTGTATCTAATCACTTCAACCGGGCGGCTCTGAGGCTGTCTGAACCAACCTTTCGA 1320

QY 1321 ACGAAACCGCGTATCCTGTGATTTTACATTAATAATTTTACAAATTGATAGCGGTGG 1380  
DB 1321 ACGAAACCGCGTATCCTGTGATTTTACATTAATAATTTTACAAATTGATAGCGGTGG 1380  
QY 1381 GCAATGTATAGGAACCTGTACGAACCTGGAGTGTGCGGAGGAGGAGTTAGTATTT 1440  
DB 1381 GCAATGTATAGGAACCTGTACGAACCTGGAGTGTGCGGAGGAGGAGTTAGTATTT 1440  
QY 1441 GTAACTGTAAACGTAGTGTGAAATGATTTTATTTTATTTTAAAAATTTCTAATGACAA 1500  
DB 1441 GTAACTGTAAACGTAGTGTGAAATGATTTTATTTTATTTTAAAAATTTCTAATGACAA 1500  
QY 1501 GTGTAAAGTAAATTAATGTACATTTATTTTAAATTATCAATTGTCGCCACCAAAAGT 1560  
DB 1501 GTGTAAAGTAAATTAATGTACATTTATTTTAAATTATCAATTGTCGCCACCAAAAGT 1560  
QY 1561 GAAATGTACATAGGCTTTTCAATGACTTCAACAGTGCAGACCTTCTTTTGAATTTA 1620  
DB 1561 GAAATGTACATAGGCTTTTCAATGACTTCAACAGTGCAGACCTTCTTTTGAATTTA 1620  
QY 1621 AGGATATATATTTTATACATATTAATTTAAATTTTAAACGACATCAATTAATGCTTTA 1680  
DB 1621 AGGATATATATTTTATACATATTAATTTAAATTTTAAACGACATCAATTAATGCTTTA 1680  
QY 1681 ACAACTTATTTTATACCTGAAATCAAAGTAACTGTAACATGCTGTGAAGATGTTTACT 1740  
DB 1681 ACAACTTATTTTATACCTGAAATCAAAGTAACTGTAACATGCTGTGAAGATGTTTACT 1740  
QY 1741 GATTTACCTTCCCTGTGAGGATTAATTTCTAATGTAAATTCAGAGTTTAAATGTGG 1800  
DB 1741 GATTTACCTTCCCTGTGAGGATTAATTTCTAATGTAAATTCAGAGTTTAAATGTGG 1800  
QY 1801 TCATTAATTAATTAAGAAACAAGTTTACGCTTCTTTTGGTAAATAATCTTATTAATTA 1860  
DB 1801 TCATTAATTAATTAAGAAACAAGTTTACGCTTCTTTTGGTAAATAATCTTATTAATTA 1860  
QY 1861 TTCAGAAATTTATTAATGTGACTATATTTTGTCCGTGTAATTAACATTAATTAATTA 1920  
DB 1861 TTCAGAAATTTATTAATGTGACTATATTTTGTCCGTGTAATTAACATTAATTAATTA 1920  
QY 1921 TATGATTAATTTCTGACATTAATTTTATGGAATTCGCTAGATTAACAATCAATCAATTT 1980  
DB 1921 TATGATTAATTTCTGACATTAATTTTATGGAATTCGCTAGATTAACAATCAATCAATTT 1980  
QY 1981 CATGTAACTCACTTCAAAAATAGTTGAATGTGTGTGATTAATATGTTAAATGTCATAA 2040  
DB 1981 CATGTAACTCACTTCAAAAATAGTTGAATGTGTGTGATTAATATGTTAAATGTCATAA 2040  
QY 2041 TTTATTAATTAATTTGACAAAGTTGCACTTAAATGTATGAATTAATTAATTTGTTTAA 2100  
DB 2041 TTTATTAATTAATTTGACAAAGTTGCACTTAAATGTATGAATTAATTAATTTGTTTAA 2100  
QY 2101 AACATTTAATTAATTTGCTGCTGCTGATTTTAAATGAATAAAGAAATTAACCCACACCT 2160  
DB 2101 AACATTTAATTAATTTGCTGCTGCTGATTTTAAATGAATAAAGAAATTAACCCACACCT 2160  
QY 2161 AATTGAAGTTTATTAATTTGCTGCTGATTAATAAAAAATCATATCAATTTTACAAAGTCA 2220  
DB 2161 AATTGAAGTTTATTAATTTGCTGCTGATTAATAAAAAATCATATCAATTTTACAAAGTCA 2220  
QY 2221 AATTGAAGTTTATTAATTTGCTGCTGATTAATAAAAAATCATATCAATTTTACAAAGTCA 2280  
DB 2221 AATTGAAGTTTATTAATTTGCTGCTGATTAATAAAAAATCATATCAATTTTACAAAGTCA 2280  
QY 2281 AATTGAAGTTTATTAATTTGCTGCTGATTAATAAAAAATCATATCAATTTTACAAAGTCA 2340  
DB 2281 AATTGAAGTTTATTAATTTGCTGCTGATTAATAAAAAATCATATCAATTTTACAAAGTCA 2340  
QY 2341 CATTTTAAAGTGTCAATTTGAGAAATTTCTGTATTAATAAATGGAATTTTATTTGAGTAT 2400  
DB 2341 CATTTTAAAGTGTCAATTTGAGAAATTTCTGTATTAATAAATGGAATTTTATTTGAGTAT 2400  
QY 2401 AATTAATCCCGCAACAGCCATTTGCAAGTTTCTACACAATTAATAACGTAATGTATCAT 2460





Db 624 TGAAGCCCGTTCGCTTTCTGTAAAGTAGAATTATAGGTGGGTGAGGCGCATGACC 683  
QY 583 TGGCGCGCATCATCGAGATGGCGGCCCATGTCCTTCTGTACGAAACMAATGTATGC 642  
Db 684 TCGGAAGAACATCAGGTTGGGGCCACAGTCCCATTTGTGCGCA---AATTGAACGG 740  
QY 643 CAACGCTGGGGGAGAGCGCACCGCTGTGGTAAAGCAATGTGGGGCCAGTGGCG--- 639  
Db 741 TACTGACAGCAGACACGGGTAGTTGAGGCGCAGACAGATGTGTGCCCCCGCTCC 800  
QY 700 -----CAGCAGACCTCCCGCAGATGCGCCGCGCCGCGTGCACGCGGGTCCACGAGGC 753  
Db 801 CTCGGGATCTCTCCGCGCGGTATGGCCGGTCCCGTGCACCCACGATATGCAATGTAGC 860  
QY 754 CGCGCGGCTCGCCACCTTCAGAGACTGCGCCAGACGTATGCGCCAAACCCGAGGAACT 813  
Db 861 CGACAGACTACGAGATTTTAAAGACTGGCCACGATGATGCAAAAACCTGAAGACT 920  
QY 814 GGCAGAGGCGCGATTTCTTCTATACAGGCCCAAGTGACAAAACGAATGCTTCTATTGGCA 873  
Db 921 CGCGAGGCTGGCTTTTCTTACACTGTGTGAGGAGACAAACCAAGTGTATTATGCGA 980  
QY 874 CGAGGGCTTAAAGATTGGGAAAGCATGACGTTCCGTGGGAAACAGACGCGCAGATGCTT 933  
Db 981 TGTGTGATTTAAAGATTGGGAAACCATGACGTAACCTTGGGAAACACACGCAAGTGT 1040  
QY 934 CGACGCGCTGCGCTAGCTGCAATTTGTGAAAGACGTGACTACATTCAGAGGTGAATGC 993  
Db 1041 TGACCGTTGGCTTACGTGCAATTGGTGAAGGGTCGAGAAATACGTTCAAAAGGTGATTTC 1100  
QY 994 GGAAGGCACTGCAATCTGTCTAGCCAGAAAGAACAG-----CGCCACCAATGA 1044  
Db 1101 TGAAGCTTGTAGAGTATCCCGTCAAGAAAGGAAAGATGATGAGCAACCCGACGACTGC 1160  
QY 1045 TTGCACTAAGAAAGTGGCCCAAGAGGGCGAGAAACATTTGATGACTTAAATPATGTAA 1104  
Db 1161 CGAGCCAAAGCCCGCAGACAGAGGCGCCAGAAACCTACGTGATGATCTAAAGTTGTATA 1220  
QY 1105 AATATGTTATTCGAGAGAGCGTAACGTGTCTTGTGCGCGCCACGTGTGTGCGTG 1164  
Db 1221 AATCTGTATGCTGAAGAGCGTAACGTGTCTTGTGCGCGCCACGTGTGTGCGTG 1280  
QY 1165 CGCAGAGTGGCGCTGTGCAAGCAAGTCCCGATGTGTGCGAGACGTTCAAGATGC 1224  
Db 1281 CGCAGAGTGGCGCTGTGCGCGCCAGCAAGTCCCGCATGTGTGCGAGACGTTCAAAATGC 1340  
QY 1225 GGTGGGCTCTACTCTTCGCGTGAAGAGCCCTCC 1257  
Db 1341 AGTGGGTTATTTCTCTGTGAAGAGCCACC 1373

RESULT 2  
US-09-502-528-2  
; Sequence 2, Application US/09502528  
; GENERAL INFORMATION:  
; APPLICANT: Hammock, Bruce D.  
; APPLICANT: Huang, Qihong  
; APPLICANT: Maeda, Susumu  
; APPLICANT: The Regents of the University of California  
; TITLE OF INVENTION: Inhibitors of Apoptosis  
; FILE REFERENCE: 023070-112000US  
; CURRENT APPLICATION NUMBER: US/09/502,528  
; NUMBER OF SEQ ID NOS: 7  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 2  
; LENGTH: 1134  
; TYPE: DNA  
; ORGANISM: Spodoptera frugiperda  
; FEATURE:  
; OTHER INFORMATION: Sf1AP nucleotide sequence, open reading frame  
; OTHER INFORMATION: (ORF) only

; NAME/KEY: CDS  
; LOCATION: (1)..(1134)  
; OTHER INFORMATION: Fall armyworm inhibitor of apoptosis protein  
; OTHER INFORMATION: (Sf1AP)  
US-09-502-528-2

Query Match 11.6%; Score 437.2; DB 3; Length 1134;  
Best Local Similarity 69.7%; Pred. No. 2, 6e-93;  
Matches 643; Conservative 0; Mismatches 258; Indels 21; Gaps 3;

QY 343 CCGGTACCTGCTGCTGATGATTAACGGTATACGACATTCACCTCTCC 402  
Db 216 CTCTTATCTTTCTTTCCATGATTAACCGAACACGACACTTGGCTTCACTG 275  
QY 403 TGATATGCCGACATGCTGTGAAGAGAACTGTGAACATTTGATCAGTGGCCGT 462  
Db 276 GAGCAGATTGATATGAAAAGAGATGACGATGAAACATTTGAAAATGGCCGT 335  
QY 463 TACGTTTTGACGCGGAAACATTTGGCCCGCAAGGATCTACTACTCTGCTGCGGCA 522  
Db 336 AAGTTTCTATCCGAGACCACTTGTGAAATGATTTTACTACTGCGCGTGAAGA 395  
QY 523 CGAAGTGTCTGCTTCTTCTGTAAAGTAAATATAGGTGAGTGAAGCGACATCC 582  
Db 396 TGAAGCCGTTGGCTTTCTGTAAAGTGAAGTATAGGTGGTGAAGCGGATGACC 455  
QY 583 TGC CGCGCATCATCGAGATGGGCGCCGCGAGTGTCTTTGTACGAAACAAATGTATGC 642  
Db 456 TCGGAAGACATCAGCGTGTGGGCGCCACAGTCCCATTTGTGCGCA---AATTGAACGG 512  
QY 643 CAACGCTGGGGGAGAGCCGACCGCTGTGCTGAGACGAAATGTGGGCGCAGTGGCG--- 699  
Db 513 TACTGAGAGAGACACAGGATGTTGCGGCCAGACGAGTGTGTGCGCGCGCTCC 572  
QY 700 -----CAGCAGACCTCCCGCATGCGCCGCGCCGCGTGCACGCGGTACTCCACGAGGC 753  
Db 573 CTCGGTACTCTCTCCGCGCGGTATGGCCCGTCCCGTGCACCATGATGATCTGAAAC 632  
QY 754 CGCGCGGCTCGCCACCTTCAAGACTGGCCGAGACGTATGCGCCAAACCCGAGGAACT 813  
Db 633 CGCAGACTACGAGATTTTAAAGACTGGCCACGATCATGCGCAAAAACCTGAAGACT 692  
QY 814 GGCAGAGGCGCGATTTCTTATACAGGCCCAAGTGAACAAAGAAATGCTTCTATTGGCA 873  
Db 693 CGCGAGGCTGGCTTTTCTTATACATGCTCAGGAGACAAACCAAGTGTATTATGCGA 752  
QY 874 CGAGGGCTTAAAGATTGGGAAAGCATGACGTTCCGTGGGAAACAGCAGCCGATGCTT 933  
Db 753 TGTGTGATTTAAAGATTGGGAAACCATGACCTTGGGAAACACGCAAGTGTGTT 812  
QY 934 CGACGCGTGGCGTACGTGCAATTTGTGAAGAGACGTGACTATTCAGAGGTGAATGC 993  
Db 813 TGAACGTTGGCTTACGTGCAATTTGTGAAGGGTCGAGAAATCGTTCAAAAGTGTATTC 872  
QY 994 GGAAGGCACTGCGATTTCTGTACGAGCAAGAAACAG-----CGCCACCAATGA 1044  
Db 873 TGAAGCTTGTAGAGTATCCGCTCAAGAACGGAACCTGATGACACCCGACGACTGC 932  
QY 1045 TTGCACTAAGAAAGTGGCCCAAGAGGGCGAGAAACATTTGATGACTTAAATATGTAA 1104  
Db 933 CGAGCCAAAGCCCGCAGACAGAGGCGCCAGAAACCTACATGATGATCTAAAGTTGTATA 992  
QY 1105 AATATGTTATTCGAGAGAGCGTAACGTGTCTTGTGCGCGCCACGTGTGTGCGTG 1164  
Db 993 AATCTGTATGCTGAAGAGCGTAACGTGTCTTGTGCGCGCCACGTGTGTGCGTG 1052  
QY 1165 CGCAGAGTGGCGCTGTGCAAGCAAGTCCCGATGTGTGCGAGACGTTCAAGATGC 1224  
Db 1053 CGCAGAGTGGCGCTGTGCGCGCCAGCAAGTCCCGCATGTGCGCAGACGTTCAAAATGC 1112  
QY 1225 GGTGGGCTCTACTCTCTGTTGA 1246  
Db 1113 AGTGGGTTATTTCTCTGTGA 1134

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: November 26, 2005, 00:14:22 ; Search time 13920 Seconds  
(without alignments)  
12681.585 Million cell updates/sec

Title: US-10-041-859A-1

Perfect score: 3773  
Sequence: 1 cattataaactcacttcac.....tgcgctcactctctcgta 3773

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :  
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1: gb\_est1.\*  
2: gb\_est2.\*  
3: gb\_est3.\*  
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6: gb\_est6.\*  
7: gb\_est7.\*  
8: gb\_est8.\*  
9: gb\_est9.\*  
10: gb\_est10.\*  
11: gb\_est11.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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1	705.6	18.7	712	3	BP121000 BP121000
2	685.6	18.2	727	3	BP120885 BP120885
3	683	18.1	723	1	AV401669 AV401669
4	649.4	17.2	676	7	CK485834 CK485834
5	639.8	17.0	658	7	CK505037 CK505037
6	598.6	15.9	626	8	DN237202 DN237202
7	588.4	15.6	612	7	CK518109 CK518109
8	577	15.3	624	7	CK564268 CK564268
9	575.8	15.3	666	8	DN237481 DN237481
10	549.4	14.6	575	7	CK514550 CK514550
11	546.6	14.5	633	7	CK495885 CK495885
12	521.4	13.8	622	7	CK497882 CK497882
13	518.6	13.7	585	8	DN237482 DN237482
14	502.4	13.3	549	7	CK544469 CK544469
15	502.4	13.3	512	1	AV398511 AV398511
16	455.8	12.1	555	3	BP121882 BP121882
17	453.8	12.0	489	7	CK494236 CK494236
18	449.6	11.9	459	7	CK500174 CK500174
19	438.8	11.6	500	3	BP115618 BP115618
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21	293.6	7.8	522	7	CK516014 CK516014
22	287.2	7.6	292	8	DN237804 DN237804

23	271	7.2	624	7	CV526245	CV526245 He_wd1_09
24	196.2	5.2	201	8	DN237429	DN237429 EST00555
c 25	179.6	4.8	804	10	CG786123	CG786123 CM MBA-76
26	128.8	3.4	1133	8	DN682800	DN682800 CGX26-C05
27	121.8	3.2	130	7	CK496041	CK496041 rswb0_00
28	121	3.2	691	3	BM588815	BM588815 170006873
29	114	3.0	712	3	BM601939	BM601939 170006870
30	113.4	3.0	1359	8	DN685273	DN685273 CGX40-G12
31	112.4	3.0	1896	8	CG753083	CG753083 P048-1-C0
32	110.6	2.9	786	8	DR832669	DR832669 JGI CAB2
33	108.8	2.9	727	6	CF525095	CF525095 AGENCOURT
34	108.8	2.9	788	8	DN069067	DN069067 JGI_CABD5
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c 40	104	2.8	678	6	CA805412	CA805412 ES00118a.
c 41	102.8	2.7	1261	8	DN682799	DN682799 CGX26-C05
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c 43	102.2	2.7	1539	10	AG340947	AG340947 Mus muscu
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## ALIGNMENTS

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DEFINITION BP121000  
ACCESSION BP121000  
VERSION BP121000.1 GI:29554042  
KEYWORDS EST.  
SOURCE Bombyx mori (domestic silkworm)  
ORGANISM Bombyx mori  
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;  
Bombycoidea; Bombycidae; Bombyx.  
REFERENCE  
1 (bases 1 to 712)  
Mita, K., Morimyo, M., Shimada, T., Okano, K. and Meda, S.  
Bombyx mori CDNA (Mita, K. 2003)  
JOURNAL  
Unpublished (2003)  
COMMENT  
Contact: Mita K  
Genome Research Group  
National Institute of Agrobiological Sciences  
Owashi 1-2, Tsukuba, Ibaraki 305-8634, Japan  
Tel: 81-29-838-6120  
Fax: 81-29-838-6121  
Email: kmits@nias.affrc.go.jp  
method: uni-directional, sequence direction: sequenced from T3 primer  
(5' -> 3').  
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Best Local Similarity 99.4%; Pred. No. 1.2e-132;  
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|||||  
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ACCESSION BP120885  
VERSION BP120885.1 GI:29553920  
KEYWORDS EST.  
SOURCE Bombyx mori (domestic silkworm)  
ORGANISM Bombyx mori  
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;  
Bombycoidea; Bombycidae; Bombyx.  
1 (bases 1 to 727)  
Mita,K., Morimoto,M., Shimada,T., Okano,K. and Maeda,S.  
Bombyx mori cDNA (Mita,K. 2003)  
Unpublished (2003)  
CONTACT: Mita K  
Genome Research Group  
National Institute of Agrobiological Sciences  
Tsukuba 1-2, Tsukuba, Ibaraki 305-8634, Japan  
Tel: 81-29-838-6120  
Fax: 81-29-838-6121  
Email: kmika@nias.affrc.go.jp  
method:unl-directional, sequence direction:sequenced from T3 primer  
(5' -> 3').

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Best Local Similarity 99.0%; Pred. No. 1.3e-128;  
Matches 721; Conservative 0; Mismatches 4; Indels 3; Gaps 3;

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QY 725 CCGGTGACGCGGGGTACTCCACCGAGCGCGCGGCTGGCCACTTCAAGAGCTGAGCG 784  
Db 61 CCGGTGACGCGGGGTACTCCACCGAGCGCGCGGCTGGCCACTTCAAGAGCTGAGCG 120  
QY 785 AGACGTATGCGCCAAAACCCGAGAACTGAGAGAGCGCGGATTTCTTATACAGGCCAA 844  
Db 121 AGATGATGCGCCAAAACCCGAGAACTGAGAGAGCGCGGATTTCTTATACAGGCCAA 180  
QY 845 GGTGACAAAACGAAATGCTTCTATTTGCGACGAGAGGCTTAAAGATTTGGAAAAGCATGAC 904  
Db 181 GGTGACAAAACGAAATGCTTCTATTTGCGACGAGAGGCTTAAAGATTTGGAAAAGCATGAC 240  
QY 905 GTTCCGTGGGAAAGAGACGCGCAATGTTGACACCGCTGGCGGCTACCGTCAATTGGTGA 964  
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QY 1025 GAAACAGGCGCGCAACCAATGATTCAGTGAACGTCGCCCAAGAGGCGGAAACATTTG 1084  
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QY 1085 GATGACTCTTAAATATGTTAAATATGTTATTCGAGAGAGGCTAACCGTGTCTTCTGCGCG 1144  
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QY 1145 TGGCGCACAGTGTGCGTGCAGCAAGTGCAGCTGTCAGACGACAAATGCCCATGTGT 1204  
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QY 1383 AATGTATA 1390  
Db 720 AATGTATA 727

RESULT 3  
AV401669 723 bp mRNA linear EST 01-MAR-2005  
LOCUS AV401669 Bombyx mori C108 spinning stage day-0 Bombyx mori cDNA  
DEFINITION clone hes00025 T3, mRNA sequence.  
ACCESSION AV401669  
VERSION AV401669.1 GI:6905321  
KEYWORDS EST.  
SOURCE Bombyx mori (domestic silkworm)

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 25, 2005, 22:06:22 ; Search time 2086 Seconds  
(without alignments)  
12054.595 Million cell updates/sec

Title: US-10-041-859A-1  
Perfect score: 3773  
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Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 4996997 seqs, 3332346308 residues

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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12: geneseqn2004as: \*  
13: geneseqn2004bs: \*  
14: geneseqn2005s: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	130.4	3.5	794	6	ABLS5635
5	111.8	3.0	8056	8	ABZ10246
6	109.8	2.9	8056	8	ABZ10246
7	105.6	2.8	1304	5	AAC84527
8	105.6	2.8	1317	5	AAC84520
9	105.6	2.8	1317	5	AAC84529
10	105.6	2.8	1317	5	AAC84521
11	105.6	2.8	1317	5	AAC84522
12	105.6	2.8	1317	5	AAC84522
13	105.6	2.8	1317	5	AAC84526
14	105.6	2.8	1317	5	AAC84528
15	105.6	2.8	1317	5	AAC84528
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19	104	2.8	2013	4	ABL10083

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21	104	2.8	14250	4	ABL21060	Ab121060 Drosophi1
22	101	2.7	2131	14	ADZ71009	Adz71009 Human chr
23	96.4	2.6	110000	13	ABD32968_6	Continuation (7 of
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25	94.6	2.5	5979	4	AAS45313	Aas45313 Chemical
26	94.6	2.5	5979	6	ABK28152	Abk28152 DNA trans
27	94.2	2.5	8056	6	ABZ10100	Abz10100 Haematopo
28	91.8	2.4	672	6	AAL42857	Aal42857 Survivin-
29	91.8	2.4	723	6	AAL42856	Aal42856 Survivin-
30	91.8	2.4	843	6	AAL42858	Aal42858 Survivin-
31	91.8	2.4	843	4	AAF24857	Aaf24857 Nucleotid
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34	91.8	2.4	1260	12	ADH89535	Adh89535 Human Liv
35	91.8	2.4	1260	14	AEA36171	Aea36171 Human nuc
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38	91.8	2.4	1322	10	ACC72843	Acc72843 Human can
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ALIGNMENTS

RESULT 1	ABQ78228	ABQ78228 standard; cDNA; 3773 BP.
ID	ABQ78228;	
AC	ABQ78228;	
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DT		
XX		
DE	Nucleotide sequence of inhibitor of apoptosis protein BmiAP.	
XX		
KW	Inhibitor of apoptosis protein; IAP; BmiAP; silkworm; apoptosis; insect;	
XX	Spodoptera frugiperda; insulin-resistant plant; caspase; gene; ss.	
OS	Bombyx mori.	
XX		
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PN	W0200253586-A2.	
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PA	(BURN-) BURHAM INST.	
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PI	Maeda S, Huang Q, Reed JC, Deveraux QL;	
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DR	WPI; 2002-590628/63.	
XX	P-PSDB; ABB78046.	
XX		
PT	Novel recombinant polypeptide, inhibitor of apoptosis protein family	
XX	member BmiAP from silkworm Bombyx mori BmV cells, useful for inhibiting	
PT	apoptosis and identifying an agent that modulates activity of	
XX	polypeptide.	
XX		
PS	Claim 8; Page 29-30; 62pp; English.	
XX		

CC The present score encodes a polypeptide which is an inhibitor of  
CC apoptosis protein (IAP) family member, and designated Bmi1p. Bmi1p is  
CC derived from silkworm Bombyx mori Bmi1 cells. The Bmi1p polypeptide  
CC contains two baculoviral IAP repeat (BIR) domains, followed by a RING  
CC domain. Bmi1p polypeptides and polymucleotides are useful for inhibiting  
CC apoptosis in insect cells, especially Spodoptera frugiperda or Bombyx  
CC mori cells, and mammalian cells, and plant cells. They are also useful  
CC for generating a biotic or abiotic insect-resistant plant. Bmi1p is also  
CC useful for inhibiting caspases  
XX

Sequence 3773 BP; 1108 A; 785 C; 866 G; 1014 T; 0 U; 0 Other;

Query Match 100.0%; Score 3773; DB 6; Length 3773;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 3773; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1321 ACGAAACGCGTATCCTGTGATTTTTCATTAATTAATTAATTAATTAATTAATTAATTA 1380
QY 1381 GCAATGTATAGGAATCTGTCAGAACTCGGAGTTGACGTGAGAGAGAGTTAGTATTT 1440
DB 1381 GCAATGTATAGGAATCTGTCAGAACTCGGAGTTGACGTGAGAGAGAGTTAGTATTT 1440
QY 1441 GTAACTGTAAACGTAGTTGAAATGATTTTATTTATTTATTTATTTATTTATTTATTT 1500
DB 1441 GTAACTGTAAACGTAGTTGAAATGATTTTATTTATTTATTTATTTATTTATTTATTT 1500
QY 1501 GTGTAAGTAAATTAATGATCATATTAATTTTAAGTTATCACTTTGTCACCGCAAAAGT 1560
DB 1501 GTGTAAGTAAATTAATGATCATATTAATTTTAAGTTATCACTTTGTCACCGCAAAAGT 1560
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DB 1561 GAAATGTACATAGGTTTTCATATCACTTCAACAGTCAAGACCTTCTTTTGAATTTA 1620
QY 1621 AGGATATATTTATTAATCATATTAATTAATTTTAAGAGCATCAATTAATGATTTA 1680
DB 1621 AGGATATATTTATTAATCATATTAATTAATTTTAAGAGCATCAATTAATGATTTA 1680
QY 1681 ACACTTATTTATTAACATGAATCAAGTGAAGTGAACATGCTGTAAGAAATGTTTACT 1740
DB 1681 ACACTTATTTATTAACATGAATCAAGTGAAGTGAACATGCTGTAAGAAATGTTTACT 1740
QY 1741 GATTTCACTTCCCTGTTGAAGTATTAATTTCTAATGTTAAATCCAGAGTTTAAATGTG 1800
DB 1741 GATTTCACTTCCCTGTTGAAGTATTAATTTCTAATGTTAAATCCAGAGTTTAAATGTG 1800
QY 1801 TCATATTAATTAATTAAGAAACAGTTTACGCTTTTTCCTTGAAGAAATCTTATTAATTA 1860
DB 1801 TCATATTAATTAATTAAGAAACAGTTTACGCTTTTTCCTTGAAGAAATCTTATTAATTA 1860
QY 1861 TTCAGAAATTAATTAATGACTATATTTGTTCTGTAAATTAACATTAATATATATAT 1920
DB 1861 TTCAGAAATTAATTAATGACTATATTTGTTCTGTAAATTAACATTAATATATATAT 1920
QY 1921 TATGATTAATTTGACATTAATTAATGCAATTCGTAAGATCAATCAATATCTTATTT 1980
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GenCore version 5.1.6  
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OM protein - nucleic search, using frame\_plus.p2n model

Run on: November 26, 2005, 20:56:58 / Search time 131 Seconds  
(without alignments)  
392.507 Million cell updates/sec

Title: US-10-041-859A-2  
Perfect score: 1887  
Sequence: 1 MELTKVAKKGAATLVMLKN.....TDKCPMCRPTTNVAVLYFS 346

Scoring table:  
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Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 3205263 seqs, 74304013 residues  
Total number of hits satisfying chosen parameters: 6410526

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:  
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-TRANS=human40.csl -LIST=45 -DOCALLIGN=200 -THR SCORE=pct -THR MAX=100  
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-MAXLEN=200000000 -USER=US10041859 @CGN\_1\_1\_121@runat\_23112005\_100429\_13242  
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-LONGLOG -DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5  
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Database : Published\_Applications\_NA\_New.\*  
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6: /cg21\_6/ptodata/2/pubpna/PCT\_NEW\_PUB.seq.\*  
7: /cg21\_6/ptodata/2/pubpna/US11\_NEW\_PUB.seq.\*  
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9: /cg21\_6/ptodata/2/pubpna/US11\_NEW\_PUB.seq.\*  
10: /cg21\_6/ptodata/2/pubpna/US60\_NEW\_PUB.seq.\*

SUMMARIES

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No.	Score	Query Match	Length	DB ID	Description
1	360	19.1	769	US-11-135-855-22	Sequence 22, Appl
2	326	17.3	1068	US-11-135-855-21	Sequence 21, Appl
3	98.5	5.2	1725	US-10-821-234-772	Sequence 772, Appl
4	88.5	4.7	5682	US-11-059-982-2	Sequence 2, Appl
5	86.5	4.6	1167	US-10-858-730-169	Sequence 169, Appl
6	85	4.5	2238	US-10-858-730-262	Sequence 262, Appl
7	84.5	4.5	2240	US-11-064-769-18	Sequence 18, Appl
8	84	4.5	1971	US-10-131-826A-225	Sequence 225, Appl

9	83	4.4	1899	1	US-10-689-742-77	Sequence 77, Appl
C 10	82	4.3	1611	1	US-10-980-388-2	Sequence 2, Appl
C 11	82	4.3	1612	1	US-10-980-388-51	Sequence 51, Appl
C 12	82	4.3	3369	1	US-10-821-234-805	Sequence 805, Appl
C 13	81.5	4.3	1719	1	US-10-821-234-438	Sequence 438, Appl
C 14	81	4.3	3515	1	US-10-821-234-65	Sequence 65, Appl
C 15	79.5	4.2	1740	1	US-10-689-742-53	Sequence 53, Appl
C 16	79.5	4.2	3378	1	US-10-821-234-592	Sequence 592, Appl
C 17	79	4.2	1659	7	US-11-135-855-11	Sequence 11, Appl
C 18	78.5	4.2	3109	1	US-10-821-234-63	Sequence 63, Appl
C 19	78.5	4.2	5253	9	US-11-004-057-3	Sequence 3, Appl
C 20	78.5	4.2	8910	1	US-10-821-234-281	Sequence 281, Appl
C 21	77.5	4.1	2736	1	US-10-821-234-55	Sequence 55, Appl
C 22	77	4.1	1482	9	US-11-082-389-197	Sequence 197, Appl
C 23	77	4.1	1932	7	US-11-137-465-21	Sequence 21, Appl
C 24	77	4.1	1956	1	US-10-821-234-628	Sequence 628, Appl
C 25	77	4.1	11337	1	US-10-499-715-1	Sequence 1, Appl
C 26	76	4.0	3734	1	US-10-131-826A-147	Sequence 147, Appl
C 27	76	4.0	5468	1	US-10-821-234-49	Sequence 49, Appl
C 28	76	4.0	43948	1	US-10-949-720-393	Sequence 393, Appl
C 29	75.5	4.0	987	1	US-10-821-234-819	Sequence 819, Appl
C 30	75	4.0	1731	7	US-11-074-176-183	Sequence 183, Appl
C 31	75	4.0	3721	1	US-10-131-826A-543	Sequence 543, Appl
C 32	75	4.0	3911	9	US-11-004-057-5	Sequence 5, Appl
C 33	75	4.0	4351	1	US-10-821-234-295	Sequence 295, Appl
C 34	74.5	3.9	1284	7	US-11-074-176-363	Sequence 363, Appl
C 35	74.5	3.9	1399	7	US-11-182-592-5	Sequence 5, Appl
C 36	74.5	3.9	2058	7	US-10-967-527A-1	Sequence 1, Appl
C 37	74.5	3.9	2058	7	US-11-065-943-57	Sequence 57, Appl
C 38	74.5	3.9	2388	1	US-10-821-234-252	Sequence 252, Appl
C 39	74	3.9	2112	1	US-10-821-234-465	Sequence 465, Appl
C 40	74	3.9	2754	1	US-10-821-234-163	Sequence 163, Appl
C 41	73.5	3.9	2737	1	US-10-131-826A-55	Sequence 55, Appl
C 42	73	3.9	1854	9	US-11-082-389-133	Sequence 133, Appl
C 43	72.5	3.8	4338	1	US-10-526-731-2	Sequence 2, Appl
C 44	72	3.8	1503	1	US-10-131-826A-363	Sequence 363, Appl
C 45	72	3.8	1546	8	US-11-112-944-14	Sequence 14, Appl

ALIGNMENTS

RESULT 1  
US-11-135-855-22 Application US/11135855  
Publication No. US20050255557A1  
GENERAL INFORMATION:  
APPLICANT: SMITHKLINE BEECHAM CORPORATION  
APPLICANT: SMITHKLINE BEECHAM P.L.C.  
TITLE OF INVENTION: NOVEL COMPOUNDS  
FILE REFERENCE: GPS0013  
CURRENT APPLICATION NUMBER: US/11/135,855  
CURRENT FILING DATE: 2005-05-24  
PRIOR APPLICATION NUMBER: US/10/203,708  
PRIOR FILING DATE: 2002-08-13  
PRIOR APPLICATION NUMBER: PCT/US01/04703  
PRIOR FILING DATE: 2001-02-14  
PRIOR APPLICATION NUMBER: 60/182,172  
PRIOR FILING DATE: 2000-02-14  
PRIOR APPLICATION NUMBER: 60/186,084  
PRIOR FILING DATE: 2000-02-29  
NUMBER OF SEQ ID NOS: 46  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 22  
LENGTH: 769  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-11-135-855-22  
Alignment Scores:  
Pred. No.: 360.00 Length: 769  
Score: 47.78% Matches: 91  
Percent Similarity: 47.78% Conservative: 38  
Best Local Similarity: 33.70% Mismatches: 103

Query Match: 19.08% Indels: 40  
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QY 102 LeuGlyAArgGlyAArgGlyUValCyvCyvAlaPheCyvLyValGluIleMetAArgTPVal 121  
DB 1 ATGGGACCTAAAGACAGTGCACAGTGCCTGACCGTGCACAGCCGACCACTGGGCA 60  
QY 122 GluGlyAAspAAspProAlaAlaAspHisAArgAArgTPAlaPro-----GlnCyv 137  
DB 61 GCCGGTGAATGATGCTCCACGACGAGAG---CGCTG-TGACACCCGCTCTGTGGGACGCTGT 116  
QY 138 Pro-----PheValAArgLyvGlnMetTyAlaAsnAlaGlyGlyGlu 151  
DB 117 CTTAGGCTTGACACCTGCAGAGCTGCAGACCAAGTGAATGGGACATCTGGGCGACGT 176  
QY 152 AlaThr-----AlaValGlyAArg-AArgGlyCyvGlyAlaSerAlaAlaThrGlnProPr 169  
DB 177 GCGGCCCCGTGACAGAGAGAGAGAGAGGCGCGCGGGCCACCTTGTCCAGGGGGCC 236  
QY 169 oArgMetProGlyProValHisAlaAArgTyrsSerThrGluAlaAlaAArgLeuAlaThrPh 189  
DB 237 TGCTTCCCGGCG-----ATGGGCTTGAGAGAGTGGCTGTGGCTTCTT 281  
QY 189 eLyvAAspTPProAArgAArgMetAArgGlnLyvProGluGluLeuAlaGlyUValAArgPhePh 209  
DB 282 CTATGACTGGCCGCTGACTGCTGAGTGCACCCGAGACTGCTGCTGCTGCTGGCTTCTT 341  
QY 209 eTyThrGlyGlyGlnGlyAAspLyvThyTyvCyvPheTyvCyvAAspGlyGlyLeuLyvAAspTr 229  
DB 342 CCACACAGGCGCATCAGAGACAAAGGTGAAGTGTCTTCTGCTATGCGGGCGCTGCAGAGACTG 401  
QY 229 pGluSerAAspAAspValProTyrGluGlnHisAlaAArgTyrsThrPheAAspAArgCyvAlaTyvA 249  
DB 402 GAAGCCCGGGGAGACCCCTGCAGAGCAATGCCAGATGGGTGTCCTCC--TGTCAATGCTCT 459  
QY 249 GlnLeuValLyvGlyAArgAAspTyvTyrIleGlnLyvValLyvSerGlyUValAThrAlaIleSe 269  
DB 460 GCTCGCGGTCAAAAGAGAGAGACTTGTGCCACAGTGTGCAGAGACTCACTCCAGACTGCT 519  
QY 269 rAlaSer-----GluGluGluGlnAlaAlaThrAAspSerThyLyvAAs 284  
DB 520 GGGCTCTTGAGACCCGTGGGAGAGACCGGAGAGCGAGCCCT-----562  
QY 284 nValAlaGlnGluGlyGlu-----LysHisLeuAAspAAspSerLy 297  
DB 563 -GTGGCCCTCCGGAGCCAGGAGATGTGAGGCGGAGCTGGCGGGCTGCAGAGAGAG 621  
QY 297 sIleCyvLyvIleCyvTyrsSerGluGluAArgAAsnValCyvPheValProCyvGlyHisAAs 317  
DB 622 GACGTGCAGAGTGTGCTGCTGACCGCGCGGTGCATGTTTGTGCTCGCGGCGGCACT 681  
QY 317 lValAlaCyvAlaLyvCyvAlaLeuSerThyAAspLyvCyvProMetCyvAArgAArgThyPh 337  
DB 682 GGTCC--TGTGCTGAATGTGTGCCCCCGGCTGCAGACTGTGCCCCATGTGCAGAGCCCCCG 738  
QY 337 eThrAAsnAlaValAArgLeuTyvPheSer 346  
DB 739 CCGCAGCCCGGTGCGACCTTCTGTC 766  
RESULT 2  
US-11-135-855-22  
; Sequence 21, Application US/1135855  
; Publication No. US2005025557A1  
; GENERAL INFORMATION:  
; APPLICANT: SMITHKLINE BEECHAM CORPORATION  
; APPLICANT: SMITHKLINE BEECHAM P.L.C.  
; TITLE OF INVENTION: NOVEL COMPOUNDS  
; FILE REFERENCE: GP50013  
; CURRENT APPLICATION NUMBER: US/11/135,855  
; CURRENT FILING DATE: 2005-05-24  
; PRIOR APPLICATION NUMBER: US/10/203,708

; PRIOR FILING DATE: 2002-08-13  
; PRIOR APPLICATION NUMBER: PCT/US01/04703  
; PRIOR FILING DATE: 2001-02-14  
; PRIOR APPLICATION NUMBER: 60/182,172  
; PRIOR FILING DATE: 2000-02-14  
; PRIOR APPLICATION NUMBER: 60/186,084  
; PRIOR FILING DATE: 2000-02-29  
; NUMBER OF SEQ ID NOS: 46  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 21  
; LENGTH: 1068  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; US-11-135-855-21  
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Pred. No.: 2,56e-23 Length: 1068  
Score: 326.00 Matches: 89  
Percent Similarity: 36.54% Conservative: 44  
Best Local Similarity: 24.45% Mismatches: 104  
Query Match: 17.28% Indels: 128  
DB: 7 Gaps: 10  
US-10-041-859A-2 (1-346) x US-11-135-855-21 (1-1068)  
QY 102 LeuGlyAArgGlyAAspGlyUValCyvCyvAlaPheCyvLyvValGluIleMetAArgTPVal 121  
DB 1 ATGGGACCTAAAGACAGTGCACAGTGCCTGCACCGTGCACAGCCGACCACTGGGCA 60  
QY 122 GluGlyAAspAAspProAlaAlaAspHisAArgAArgTPAlaPro-----GlnCyv 137  
DB 61 GCCGGTGAATGATGCTCCACGACGAGAG---CGCTG-TGACACCCGCTCTGTGGGACGCTGT 116  
QY 138 Pro-----PheValAArgLyvGlnMetTyAlaAsnAlaGlyGlyGlu 151  
DB 117 CTTAGGCTTGACACCTGCAGAGCTGCAGACCAAGTGAATGGGACATCTGGGCGACGT 176  
QY 152 AlaThr-----AlaValGlyAArg-AArgGlyCyvGlyAlaSerAlaAlaThrGlnProPr 169  
DB 177 GCGGCCCCGTGACAGAGAGAGAGAGAGGCGCGGGCGCACCTTGTCCAGGGGGCC 236  
QY 169 oArgMetProGlyProValHisAlaAArgTyrsSerThrGluAlaAlaAArgLeuAlaThrPh 189  
DB 237 TGCTTCCCGGCG-----ATGGGCTTGAGAGAGTGGCTGTGGCTTCTT 281  
QY 189 eLyvAAspTPProAArgAArgMetAArgGlnLyvProGluGluLeuAlaGlyUValAArgPhePh 209  
DB 282 CTATGACTGGCCGCTGACTGCTGAGGTGCACCCGAGCTGCTGCTGCTGGCTTCTT 341  
QY 209 eTyThrGlyGlyGlnGlyAAspLyvThyTyvCyvPheTyvCyvAAspGlyGlyLeuLyvAAspTr 229  
DB 342 CCACACAGGCGCATCAGAGACAAAGGTGAAGTGTCTTCTGCTATGCGGGCGCTGCAGAGACTG 401  
QY 229 pGluSerAAspAAspValProTyrGluGlnHisAlaAArgTyrsThrPheAAspAArgCyvAlaTyvA 249  
DB 402 GAAGCCCGGGGAGACCCCTGCAGAGCAATGCCAGATGGGTGTCCTCCAGACTGCAATGCTCT 461  
QY 249 GlnLeuValLyvGlyAArgAAspTyvTyrIleGlnLyvVal-----261  
DB 462 GCTCGCGGTCAAAAGAGAGACTTGTGCCACAGTGTGCAGAGACTCACTCCAGACTGCT 521  
QY 261 -----261  
DB 522 GGGCTCTGGGTGAGGCGCACCTTCTGCGGGGCTCCGGGTGCAGTGGGCTCTGCCCC 581  
QY 261 -----261  
DB 582 TCTATTTCACAGGCTGATGTCGTGCTCTTCCAGAGCCGCTGGAAGAACGG 641  
QY 262 -----LysSerGluAlaTh 266  
DB 642 AAGAGCAGCCCTGTGCGCCCTCCGCTCAGTGTGAAGTGTCCAGAGGCGCAGGTGCA 701



GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model

Run on: November 26, 2005, 19:40:17 ; Search time 942 Seconds  
(without alignments)  
3037.372 Million cell updates/sec

Title: US-10-041-859A-2  
Perfect score: 1887  
Sequence: 1 MEITKAKKAGAAATLVMLKN.....TDKPCMCRRFTNAVLRYFS 346

Scoring table:  
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Searched: 9793542 segs, 4134689005 residues  
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Listing first 45 summaries

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-DEV.TIMEOUT=120 -MAIN.TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database: Published Applications\_NA\_Main.\*  
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8: /cg2\_6/ptodata/1/pubpna/US10D\_PUBCOMB.seq:\*  
9: /cg2\_6/ptodata/1/pubpna/US10E\_PUBCOMB.seq:\*  
10: /cg2\_6/ptodata/1/pubpna/US11\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	787	41.7	50000	8 US-10-706-635-23	Sequence 23, Appli
3	748	39.6	794	8 US-10-706-635-4	Sequence 4, Appli
4	719.5	38.1	1317	7 US-10-267-502-402	Sequence 202, App
5	719.5	38.1	1858	10 US-11-097-143-28832	Sequence 28832, A
6	719.5	38.1	2013	10 US-11-097-143-12365	Sequence 12365, A
7	719.5	38.1	10432	10 US-11-097-143-12364	Sequence 12364, A

8	719.5	38.1	14250	10 US-11-097-143-28831	Sequence 28831, A
9	526.5	27.9	2563	6 US-10-305-720-1076	Sequence 1076, Ap
10	526.5	27.9	2563	7 US-10-641-643-894	Sequence 894, App
11	526.5	27.9	2563	9 US-10-485-225-63	Sequence 63, Appli
12	526.5	27.9	2601	6 US-10-232-286-3	Sequence 3, Appli
13	526.5	27.9	2601	8 US-10-934-717-3	Sequence 3, Appli
14	526.5	27.9	3076	3 US-09-954-456-1635	Sequence 1635, Ap
15	526.5	27.9	3076	3 US-09-954-531-16	Sequence 16, Appli
16	526.5	27.9	3076	5 US-10-197-290-1	Sequence 1, Appli
17	526.5	27.9	3076	6 US-10-388-263-157	Sequence 157, App
18	526.5	27.9	3076	7 US-10-776-827-11	Sequence 11, Appli
19	526.5	27.9	3076	9 US-10-843-641A-1083	Sequence 1083, Ap
20	526.5	27.9	3076	9 US-10-843-641A-4662	Sequence 4662, Ap
21	526.5	27.9	3076	10 US-11-048-271-1	Sequence 1, Appli
22	526.5	27.9	3164	6 US-10-141-618-5	Sequence 5, Appli
23	526.5	27.9	3165	6 US-10-269-909-5	Sequence 5, Appli
24	526.5	27.9	3165	6 US-10-172-118-564	Sequence 564, App
25	526.5	27.9	3165	6 US-10-366-307-5	Sequence 5, Appli
26	526.5	27.9	3165	7 US-10-342-887-564	Sequence 564, App
27	526.5	27.9	5212	8 US-10-825-282-39	Sequence 39, Appli
28	526.5	27.9	5844	3 US-09-971-392-253	Sequence 253, App
29	526.5	27.9	5857	6 US-10-247-671-18	Sequence 18, Appli
30	525.5	27.8	2673	8 US-10-462-952-2	Sequence 2, Appli
31	525.5	27.8	2676	3 US-09-974-592-11	Sequence 11, Appli
32	525.5	27.8	6659	3 US-09-974-592-5	Sequence 5, Appli
33	525.5	27.8	6659	7 US-10-636-065-230	Sequence 230, App
34	524.5	27.8	1815	9 US-10-975-974-53	Sequence 53, Appli
35	524.5	27.8	2676	3 US-09-201-936-5	Sequence 5, Appli
36	524.5	27.8	2676	7 US-10-636-065-220	Sequence 220, App
37	524.5	27.8	2676	7 US-10-600-272-5	Sequence 5, Appli
38	524.5	27.8	2916	7 US-10-240-425-1436	Sequence 1436, Ap
39	524.5	27.8	2916	7 US-10-776-827-31	Sequence 31, Appli
40	517.5	27.4	2450	3 US-09-201-936-39	Sequence 39, Appli
41	517.5	27.4	2474	7 US-10-636-065-226	Sequence 226, App
42	517.5	27.4	2474	7 US-10-600-272-39	Sequence 39, Appli
43	514.5	26.3	3153	8 US-10-482-952-10	Sequence 10, Appli
44	507.5	26.9	1857	9 US-10-975-974-47	Sequence 47, Appli
45	507.5	26.9	2580	3 US-09-201-936-7	Sequence 7, Appli

## ALIGNMENTS

RESULT 1  
US-10-041-859-1  
Sequence 1, Application US/10041859  
Publication No. US20030049796A1  
GENERAL INFORMATION:  
APPLICANT: HUANG, QIHONG  
APPLICANT: REED, JOHN C.  
APPLICANT: DEVERAUX, QUINN L.  
TITLE OF INVENTION: INHIBITOR OF APOPTOSIS PROTEINS AND NUCLEIC ACIDS AND  
FILE REFERENCE: 087102/027 2537  
CURRENT APPLICATION NUMBER: US/10/041, 859  
CURRENT FILING DATE: 2002-01-07  
PRIOR APPLICATION NUMBER: 60/260,478  
PRIOR FILING DATE: 2001-01-08  
NUMBER OF SEQ ID NOS: 25  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 1  
LENGTH: 3773  
TYPE: DNA  
ORGANISM: Bombyx mori  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (2733)..(3770)  
US-10-041-859-1  
Alignment Scores:  
Pred. No.: 1.84e-208  
Score: 1887.00  
Percent Similarity: 100.00%  
Length: 3773  
Matches: 346  
Conservative: 0

Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	5	Gaps:	0

QY	MetGluLeuThrIleuValAlaIleuAsnGlyAlaAlaIleuThrLeuValMetLeuIleuAsn	20
Db	ATGGAGTTGACGAAAGTTGCTTAATAATGAGAGCTCCGCGACGTTGTATGTTAAAAAT	206
QY	AlaArgAspAlaIleuMetArgProPheIleGlyProLeuMetLeuSerSerCysGluSer	40
Db	GCGGGGAGTGCAAAATCGACCTTTCATTGGTCCGCTCATGTTATCTCGGTGAGACT	266
QY	SerThrThrSerThrIleuProSerProSerSerSerAlaAspIleThrAspAsnHisAsp	60
Db	TCAACGACATCCACACTCCCGCTCACCTTCGTCAGCTGATTAATAACGATATACACAC	326
QY	ThrPheAsnPheLeuProAspMetProAspMetArgAspGluGluGluAlaArgLeuIleThr	80
Db	ACATTCACTTCCTCTCTGATATATGCCACATGCGCTGTAAAGAGAACGCTTGAAAACA	386
QY	PheAspGlnTrpProValThrPheLeuThrProGluGluLeuAlaArgAsnGlyPheIle	100
Db	TTTGATCAGTGAGCCCGTTACGTTTGTGACGCCGGAACAATTGGCCCGAACGGAATTCAC	446
QY	TyrLeuGluIleArgGlyAspGluValCysCysValaPheCysIleValGluIleMetArgTrp	120
Db	TACCTCGGTCGCGGGAGCAAGGTGCGTGCTTTCTGTAAAGTAAGAAATTATGAGGTGG	506
QY	ValGluGlyAspAspProAlaAlaAspHisArgArgTrpAlaProGluIleCysProPheVal	140
Db	GTCCAGGCGACGACATCTCTGCGCGCATATCGAGATATGGCGCCCAATGCTCTTTGTA	566
QY	ArgIleuGlnMetTyrAlaAsnAlaGlyIleGluAlaThrAlaValaGlyIleArgAspGluCys	160
Db	CGAAAACAAAGTATGATGCCACGCTGGGGAGAGCGGACCGGCTGTGGTAAAGACGAAGT	626
QY	GlyIleAspAlaAlaThrGlnProProArgMetProGlyProValHisAlaArgTyrSer	180
Db	GGGGCGAATGGGGCCACGACGCTCCGCGATGCCCGGCCCGCGTGACGCGGATCTCC	686
QY	ThrGluAlaAlaArgLeuAlaThrPheIleuAspTrpProArgArgMetArgGlnIleAspPro	200
Db	ACCGAGGCGCGCGGCTCGCCACCTTCAAGAGCTGCGCGAAGCATGCGCCAAAACCC	746
QY	GluGluLeuAlaGluAlaGlyPhePheTyrThrGlyGlnIleAspIleThrIleCysPhe	220
Db	GAGGAACCTGGCAGAGCGCGGATCTCTTATACAGCCCAAGGTGACAAAACCAAAATGCTTC	806
QY	TyrCysAspGlyIleGlyLeuIleuAspTrpIleSerAspAspValProTrpGluGlnHisAla	240
Db	TATTCGACGAGGGCTAAAGATTGGGAAAGCGATGACGTTCCGTGGAAACAGACCC	866
QY	ArgTrpPheAspArgCysAlaIleTyrValGlnLeuValIleuGlyIleArgAspTyrIleGlnIle	260
Db	AGATGCTTCGACCGCTGCGCGTACGTGCATTGGTGAAGAGACGTGACTTACATTCAGAG	926
QY	ValIleuSerGluAlaThrAlaIleSerAlaSerGluGluGluGlnAlaAlaThrAsnAsp	280
Db	GTGAAGTCGAGGCGCACCTGCGATATCTGTACGGAAGAAAGAACGCGCCACCAATGAT	986
QY	SerThrIleuAsnValaIleGlnGluIleGlyIleuIleuHisIleuAspAspSerIleIleCysIle	300
Db	TCGACTTAAGACGTGCCCAAGGCGCAGAAACATTGGATGACTCTTAATAATATGTTAA	1046
QY	IleCysTyrSerGluGluIleuArgAsnValCysPheValProCysGlyIleValaIleAlaCys	320
Db	ATATGTTATTCGAGAGCGTATACGTGACTTCGAGCGGTGGGCACTGCTGGTGGCGCT	1106
QY	AlaIleuCysValaIleuSerThrAspIleCysProMetCysValArgIleThrPheThrAsnAla	340
Db	GCCAAAGTCGCGCTGTCCAGACGCAACAGTGGCCGATGTGCGAGAGCACTTACAGATACG	1166

QY	341	ValArgLeuTyrPheSer	346
Db	1226	GTGGGCTCTACTTCTCG	1243

## RESULT 2

```

US-10-706-635-23/c
; Sequence 23, Application US/10706635
; Publication No. US20050014263A1
; GENERAL INFORMATION:
; APPLICANT: Moyer, Richard W.
; APPLICANT: L1, Y1
; TITLE OF INVENTION: Materials and Methods for Delivery and Expression of Heterologous
; TITLE OF INVENTION: Vertebrate Cells
; FILE REFERENCE: US-221C1XC21
; CURRENT APPLICATION NUMBER: US/10/706,635
; CURRENT FILING DATE: 2003-11-12
; PRIOR APPLICATION NUMBER: 09/086,651
; PRIOR FILING DATE: 1998-05-29
; PRIOR APPLICATION NUMBER: 09/662,254
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: 60/224,479
; PRIOR FILING DATE: 2000-08-10
; NUMBER OF SEQ ID NOS: 80
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 23
; LENGTH: 50000
; TYPE: DNA
; ORGANISM: Amsacta moorei entomopoxvirus
US-10-706-635-23

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### Alignment Scores:

Pred. No.:	7.49e-79	Length:	50000
Score:	787.00	Matches:	143
Percent Similarity:	63.82%	Conservative:	44
Best Local Similarity:	48.81%	Mismatches:	86
Query Match:	41.71%	Indels:	20
DB:	8	Gaps:	5

US-10-041-859A-2 (1-346) X US-10-706-635-23 (1-50000)

55 LysThrAspAsnHisAspThrPheAsnPheLeuProAspMetProAspMetArg----- 72

Db 24584 AAAAATACATACATATATTATATTATATTAAATATGATGATGACATTAACTTGTAT 24525

73 ArgGlUGlUGlWArgLeuLysThrPheAbpGlnTrpProValThrPheLeuThrProGlu 92

DB 24524 AATGAAATCTGAAGATACAAACATTTGAAATATGGCCCATAAATTTATTAACCTCTGAA 24465

93 GINLEWLAATGASHNGLYPHEIYIYILEUUGLYMIGLYAVRGLVALCYBVCYBMAFINE 112

[illegible]

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GenCore version 5.1.6  
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Run on: November 26, 2005, 17:44:57 ; Search time 225 Seconds  
(without alignments)  
2733.495 Million cell updates/sec

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Perfect score: 1887  
Sequence: 1 MELTKAKKGAATLVMLKN.....TDKPCMCRRFTTNVRLYFS 346

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Fgapop 6.0 , Fgapext 7.0  
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Searched: 1303057 seqs, 888780828 residues  
Total number of hits satisfying chosen parameters: 2606114

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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

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4	748	39.6	794	3	US-09-662-254B-4	Sequence 4, Appl1
5	725.5	38.4	1317	3	US-09-586-305A-2	Sequence 2, Appl1
6	723.5	38.3	1317	3	US-09-586-305A-1	Sequence 1, Appl1
7	723.5	38.3	1317	3	US-09-586-305A-3	Sequence 3, Appl1
8	717.5	38.0	1317	3	US-09-586-305A-4	Sequence 4, Appl1
9	717.5	38.0	1317	3	US-09-586-305A-5	Sequence 5, Appl1

10	715.5	37.9	1317	3	US-09-586-305A-9	Sequence 9, Appl1
11	713.5	37.8	1317	3	US-09-586-305A-10	Sequence 10, Appl1
12	712.5	37.8	1317	3	US-09-586-305A-6	Sequence 6, Appl1
13	712.5	37.8	1317	3	US-09-586-305A-7	Sequence 7, Appl1
14	704	37.3	1304	3	US-09-586-305A-8	Sequence 8, Appl1
15	526.5	27.9	2563	3	US-09-016-434-1076	Sequence 1076, App
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17	526.5	27.9	2601	3	US-08-569-749-3	Sequence 3, Appl1
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22	526.5	27.9	3076	3	US-09-814-915A-11	Sequence 11, Appl1
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24	526.5	27.9	3573	3	US-09-949-016-5007	Sequence 5007, App
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38	517.5	27.4	2450	3	US-09-201-936-39	Sequence 39, Appl1
39	517.5	27.4	2450	3	US-09-201-932-39	Sequence 39, Appl1
40	517.5	27.4	2474	3	US-09-011-356-39	Sequence 39, Appl1
41	517.5	27.4	2474	3	US-09-672-717-226	Sequence 226, App
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44	507.5	26.9	2580	3	US-09-011-356-7	Sequence 7, Appl1
45	507.5	26.9	2580	3	US-09-672-717-222	Sequence 222, App

## ALIGNMENTS

RESULT 1  
US-09-502-528-2  
; Sequence 2, Application US/09502528  
; Patent No. 6570069  
; GENERAL INFORMATION:  
; APPLICANT: Hammock, Bruce D.  
; APPLICANT: Huang, Qihong  
; APPLICANT: Maeda, Susumu  
; TITLE OF INVENTION: The Regents of the University of California  
; FILE REFERENCE: 023070-112000US  
; CURRENT APPLICATION NUMBER: US/09/502,528  
; CURRENT FILING DATE: 2000-02-10  
; NUMBER OF SEQ ID NOS: 7  
; SOFTWARE: Patentin Ver. 2.1  
; SEQ ID NO 2  
; LENGTH: 1134  
; TYPE: DNA  
; ORGANISM: Spodoptera frugiperda  
; FEATURE:  
; OTHER INFORMATION: sfiap nucleotide sequence, open reading frame  
; NAME/KEY: CDS  
; LOCATION: (1)..(1134)  
; OTHER INFORMATION: Fall armyworm inhibitor of apoptosis protein  
; OTHER INFORMATION: (SfiAP)  
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Score: 1311.00  
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Best Local Similarity: 68.51%  
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Mismatch: 57

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; Patent No. 657069
; GENERAL INFORMATION:
; APPLICANT: Hammock, Bruce D.
; APPLICANT: Huang, Qihong
; APPLICANT: Maeda, Susumu
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: Inhibitors of Apoptosis
; FILE REFERENCE: 023070-11200US
; CURRENT APPLICATION NUMBER: US/09/502,528
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 1739
; TYPE: DNA
; ORGANISM: Spodoptera frugiperda
; FEATURE:
; OTHER INFORMATION: fall armyworm inhibitor of apoptosis protein
; OTHER INFORMATION: (SfIAP) nucleotide sequence including 5' and 3'
; NAME/KEY: CDS
; LOCATION: (229)..(1362)
; OTHER INFORMATION: fall armyworm inhibitor of apoptosis protein
; OTHER INFORMATION: (SfIAP)
US-09-502-528-1
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Score: 1311.00 Matches: 248
Percent Similarity: 79.28% Conservative: 39
Best Local Similarity: 68.51% Mismatches: 57
Query Match: 69.48% Indels: 18
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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

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10: gb\_gsa2:\*  
11: gb\_gsa3:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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5	861.5	45.7	555	3	BP121882 BP121882
6	812	43.0	512	1	AV398511 AV398511
7	709.5	37.6	624	7	CV526245 He_wd1_09

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13	520	27.6	1334	4	CNSGCPW3	CR729221 Tetraodon
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17	503	26.7	2030	4	CNSOGT10	CR733861 Tetraodon
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23	486	25.8	1851	4	BC056914	BC056914 Homo sapi
24	468.5	24.7	1133	8	DN682800	DN682800 CGX26-C05
25	467	24.7	864	7	CK189215	CK189215 EST778530
26	465	24.6	2632	4	CR859301	CR859301 Pongo pyg
27	453.5	24.0	718	4	AY432429	AY432429 Aedes aeg
28	447.5	23.7	786	8	DR832669	DR832669 JGI CAB2
29	447	23.7	890	8	CX414917	CX414917 JGI_XZT56
30	446.5	23.7	887	7	CNS02150	CNS02150 AGENCOURT
31	446	23.6	771	6	CAB03224	CAB03224 ESO11a.E
32	445.5	23.6	871	8	DN012763	DN012763 JGI_CAAQ1
33	445	23.6	727	6	CF525095	CF525095 AGENCOURT
34	445	23.6	788	8	DN069067	DN069067 JGI CABD5
35	445	23.6	1045	7	CN645252	CN645252 ILLUMIGEN
36	444.5	23.6	632	7	CO844385	CO844385 LM_GMS_00
37	444	23.5	878	8	CX498117	CX498117 JGI_XZG43
38	441.5	23.4	602	8	DN009701	DN009701 JGI_CAAQ8
39	440.5	23.3	582	7	CO861048	CO861048 LM_SMS_00
40	440.5	23.3	881	6	CF265917	CF265917 AGENCOURT
41	438.5	23.2	898	8	CV814302	CV814302 AGENCOURT
42	438.5	23.2	918	8	DN039298	DN039298 JGI_CAA1
43	437	23.1	860	7	CO647969	CO647969 ILLUMIGEN
44	435	23.0	956	5	BO652590	BO652590 AGENCOURT
45	434.5	23.0	580	3	BP292682	BP292682

ALIGNMENTS

RESULT 1  
BP121000 712 bp mRNA linear EST 16-MAY-2003  
LOCUS BP121000 cen- Bombyx mori cDNA clone cen-4016, mRNA sequence.  
DEFINITION BP121000  
ACCESSION BP121000  
VERSION BP121000.1 GI:29554042  
KEYWORDS  
SOURCE  
Bombyx mori (domestic silkworm)  
ORGANISM  
Bombyx mori  
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;  
Bombycoidea; Bombycidae; Bombyx.  
REFERENCE  
1 (bases 1 to 712)  
Mita, K., Moriyasu, M., Shimada, T., Okano, K. and Maeda, S.  
Bombyx mori cDNA (Mita, K. 2003)  
Unpublished (2003)  
Contact: Mita K  
Genome Research Group  
National Institute of Agrobiological Sciences  
Owashi 1-2, Tsukuba, Ibaraki 305-8634, Japan  
Tel: 81-29-838-6120  
Fax: 81-29-838-6121  
Email: kmita@nias.affrc.go.jp  
method: uni-directional, sequence direction: sequenced from T3 primer  
(5' -> 3').

FEATURES  
source  
Location/Qualifiers  
1..712  
/organism="Bombyx mori"  
/mol\_type="mRNA"  
/db\_xref="taxon:7091"  
/clone="cen-4016"



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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: November 26, 2005, 17:39:37 ; Search time 714 Seconds  
(without alignments)  
3229,669 Million cell updates/sec

Title: US-10-041-859A-2

Perfect score: 1887  
Sequence: 1 MELTKYAKNGAATLVMLKN.....TDKPCMCRTFNAYRLYFS 346

Scoring table: BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 4996997 seqs, 3332346308 residues

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:

-MODE=frame+ p2n.model -DEV=xlh  
-Q=cgnt\_1/USFPO.epool/US10041859/runat\_23112005\_100426\_13104/app\_query.fasta.1.519  
-Db=N\_Geneseq -QMT=fastcap -SUFFIX=p2n.rng -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0  
-UNITS=bits -START=1 -END=1 -MATRIX=blisum62 -TRANS=human40.cdi -LIST=45  
-OUTALIGN=200 -THR\_SCORE=pct -THR\_MAX=100 -THR\_MIN=0 -ALIGN=15 -MODE=LOCAL  
-OUTFMT=pco -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000  
-USRR-US10041859 @CGN 1.1 727 @runat\_23112005\_100426\_13104 -NCPU=6 -ICPU=3  
-NO MAP -LARGEQUERY -NEG\_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG  
-DEV\_TIMEOUT=120 -MAPN\_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

N\_Geneseq 21: \*  
1: geneseqn1980s: \*  
2: geneseqn1990s: \*  
3: geneseqn2000s: \*  
4: geneseqn2001as: \*  
5: geneseqn2001bs: \*  
6: geneseqn2002as: \*  
7: geneseqn2002bs: \*  
8: geneseqn2003as: \*  
9: geneseqn2003bs: \*  
10: geneseqn2003cs: \*  
11: geneseqn2003ds: \*  
12: geneseqn2004as: \*  
13: geneseqn2004bs: \*  
14: geneseqn2005s: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1887	100.0	3773	6	ABQ78228 Nucleotide
2	1311	69.5	1739	5	ABD14419 Fall army
3	787	41.7	50000	6	ABL55643 AmbPV gen
4	748	39.6	794	6	ABL55635 AmbPV bac

5	721.5	38.2	1317	5	AAC84521 Drosophila
6	719.5	38.1	1317	5	AAC84520 Drosophila
7	719.5	38.1	1317	5	AAC84522 Drosophila
8	719.5	38.1	1317	12	AD007876 Fly poly
9	719.5	38.1	1858	4	ABL21061 Drosophila
10	719.5	38.1	2013	4	ABL10083 Drosophila
11	719.5	38.1	10432	4	ABL10082 Drosophila
12	719.5	38.1	14250	4	ABL21060 Drosophila
13	713.5	37.8	1317	5	AAC84523 Drosophila
14	713.5	37.8	1317	5	AAC84524 Drosophila
15	711.5	37.7	1317	5	AAC84528 Drosophila
16	709.5	37.6	1317	5	AAC84529 Drosophila
17	708.5	37.5	1317	5	AAC84525 Drosophila
18	708.5	37.5	1317	5	AAC84526 Drosophila
19	700	37.1	1304	5	AAC84527 Drosophila
20	546.5	29.0	131680	10	ADF29092 Agrotis s
21	526.5	27.9	2563	9	ADB80989 RING-SH c
22	526.5	27.9	2563	10	ACA56478 Human s1g
23	526.5	27.9	2563	11	AD131568 Human cDN
24	526.5	27.9	2563	12	AD156274 Human pol
25	526.5	27.9	2563	13	ADS83635 Human lym
26	526.5	27.9	2601	2	AAT61591 Human c-I
27	526.5	27.9	3076	2	AAT72712 Human inh
28	526.5	27.9	3076	2	AAZ41005 Human cel
29	526.5	27.9	3076	2	AAZ22096 Human cel
30	526.5	27.9	3076	6	ABL62746 Breast c
31	526.5	27.9	3076	6	ABL66325 Lung canc
32	526.5	27.9	3076	8	ABX10968 cDNA enco
33	526.5	27.9	3076	10	AD60472 Human cel
34	526.5	27.9	3164	8	ABV75363 Human CIA
35	526.5	27.9	3164	12	ADG87134 Human c1A
36	526.5	27.9	3165	12	ADH74642 cDNA enco
37	526.5	27.9	3165	13	ADR24703 Breast ca
38	526.5	27.9	3165	13	ADR67123 Human bla
39	526.5	27.9	5212	8	ABX10333 DNA enco
40	526.5	27.9	5212	13	ADU22898 Human apo
41	526.5	27.9	5243	14	ABE22769 Human col
42	526.5	27.9	5844	10	ADB47553 Human cDN
43	526.5	27.8	5857	10	ADB25614 Human cDN
44	525.5	27.8	2673	8	ABZ58100 Mouse inh
45	525.5	27.8	2676	2	AAV55042 Murine HI

## ALIGNMENTS

RESULT 1	ABQ78228	standard; cDNA; 3773 BP.
ID	ABQ78228	
XX	ABQ78228	
AC	ABQ78228	
XX	ABQ78228	
DT	22-OCT-2002	(first entry)
XX		
DE		Nucleotide sequence of inhibitor of apoptosis protein BmiAP.
XX		Inhibitor of apoptosis protein; IAP; BmiAP; silkworm; apoptosis; insect;
KW	Spodoptera frugiperda;	insult-resistant plant; caspase; gene; ss.
XX		
OS	Bombyx mori.	
XX		
FX	Key	Location/Qualifiers
FT	CDS	2733..3773
FT		/tag= a "inhibitor of apoptosis protein BmiAP"
XX		
XX	WO200253586-A2.	
XX		
PD	11-JUL-2002.	
XX		
XX	07-JAN-2002;	2002WO-US000314.
PF		ABD14419 Fall army
XX		ABL55643 AmbPV gen
PR	08-JAN-2001;	2001US-0260478P.
XX		

PA (BURN-) BURNHAM INST.  
XX Maeda S, Huang Q, Reed JC, Devereaux QJ;  
XX WPI: 2002-590628/63.  
DR P-PSDB; ABB78046.  
XX  
PT Novel recombinant polypeptide, inhibitor of apoptosis protein family  
PT member BmiAP from silkworm Bombyx mori BmN cells, useful for inhibiting  
PT apoptosis and identifying an agent that modulates activity of  
PT polypeptide.  
XX  
PS Claim 8; Page 29-30; 62pp; English.  
XX  
CC The present score encodes a polypeptide which is an inhibitor of  
CC apoptosis protein (IAP) family member, and designated BmiAP. BmiAP is  
CC derived from silkworm Bombyx mori BmN cells. The BmiAP polypeptide  
CC contains two baculoviral IAP repeat (BUR) domains, followed by a RING  
CC domain. BmiAP polypeptides and polynucleotides are useful for inhibiting  
CC apoptosis in insect cells, especially Spodoptera frugiperda or Bombyx  
CC mori cells, and mammalian cells, and plant cells. They are also useful  
CC for generating a biotic or abiotic insult-resistant plant. BmiAP is also  
CC useful for inhibiting caspases

Seq Sequence 3773 BP; 1108 A; 785 C; 866 G; 1014 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 7.58e-168 Length: 3773  
Score: 1887.00 Matches: 346  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 6 Gaps: 0

US-10-041-859A-2 (1-346) x ABQ78228 (1-3773)

QY 1 MetGluLeuThrIySvAlaAlaIySaenGlyAlaAlaIaThrlEuValNectLeuIySaN 20  
DB 206 ATGAGATTGCGAAGATTGCTTAAAAATGGAGTCGCCGCCGTTGGTGAATTAATAAT 265  
QY 21 AlaArgAspAlaIySaenArGpRopheIleGlyProLeuMetLeuSerCysGluSer 40  
DB 266 GCGCGGAGATGCAGAAATGGCACTTTCATATGTCGCCGTCAATGATTCCTGTGTGAGTCT 325  
QY 41 SerThrThrSerThrLeuProSerProSerSerSerAlaAspIySvThrAspAsnIAsp 60  
DB 326 TCACAGACATCCACACTCCCGTCACCTTCCTGTCAGCTGATTAACGATATATCAGAC 385  
QY 61 ThrPheAsnPhleuProAspMetProAspMetArGArgGluGluGluArgLeuIySvThr 80  
DB 386 ACATTCACAACTTCTTCTCTGATATGCCCCGACATCGTCGTGMAAGAGAACCTCTGAACA 445  
QY 81 PheAspGluTTrProValThrlPheLeuThrlProGluGluLeuAlaArgAsnGlyPheIy 100  
DB 446 TTTCATCAGTGGCCCGTTACGTTTGTGACCCCGAACAATGGCCGCAACGGATTTCTAC 505  
QY 101 TyrLeuGlyArGslYAspGluValCySvSaIAPheCylSvSaIyGluIleMetArGTrp 120  
DB 506 TACCTGGTGGCGGCGAGAGTGTGCTGCTTTCGTAAAGTAAGAAATATAGAGGTGG 565  
QY 121 ValGluGlyAspAspProAlaAlaAspPhIAsArgTrpAlaProGluNcySvProPheVal 140  
DB 566 GTTCGAGAGCGACATCTCTCCCGCATCGAGATGGCGGCCCAAGTGTCCCTTTGTA 625  
QY 141 ArgGlyGluMetIySvThrlaAsnAlaGlyGlyGluAlaThrlaValGlyArGAspGluCySv 160  
DB 626 CGAAACCAATGTATGCAACGCTGGGGAGAGAGCGACCGCTGTGGTAAGACGAATGT 685  
QY 161 GlyAlaSerAlaIaThrlGlnProProArGMetProGlyProValHisAlaArGTrpSer 180  
DB 686 GGGGCGAGTGGCGGCGACGAGCTCCCGCATATGCCGCCCGCGGTGACAGCGGCGTACTCC 745  
QY 181 ThrGluAlaIaIaThrlGluAlaThrlPheIyAspTrlProArgArgMetArgGluNcySvPro 200

DB 746 ACCGAGCCCGCGGCTCCGACCTTCAAGAGACTGGCCGAGACGATGTGGCAAAAACCC 805  
QY 201 GluGluLeuAlaGlyAlaIySvPheThrlGlyGluGlyAspIySvThrlYsCySvPhe 220  
DB 806 GAGAACTGGCAGAGCGCGGATTTCTTATACAGGCGAAGGTGACAAAACGAAATGCTTC 865  
QY 221 TyrCyAspGlyGlyLeuIyAspTrlGluSerAspAspValProTrlGluGluHisAla 240  
DB 866 TATTGCGAGCGAGGCGCTTAAAGATTGGAAACGATGACGTTCCGTGGGMAACAGCACGCC 925  
QY 241 ArgTrlPheAspAspCySvAlaThrlValGluLeuValIySvGlyArGAspTrlIleGluNcySv 260  
DB 926 AGATGGTTCACCGCTCGCGCTACGTCGATGTGAAAGACGTAATTCATTCAGAG 985  
QY 261 ValIySerGlyAlaIaThrlaIleSerAlaSerGluGluGluGluAlaIaThrlaAsp 280  
DB 986 GTGAATCGGAGCGCACCTCGATATCTGTACGAAAGAAAGAACAGCGCCGCAATGAT 1045  
QY 281 SerThrIySaenValaIaGluGluGlyGlyIySvHIsleuAspAspSerIySvIleCySvIySv 300  
DB 1046 TCACACTTAAGAACGTCCGCCAAGAGGCGGAGAAACATTTGGATGACTCTTAAAAATATGTAA 1105  
QY 301 IleCysTrSerGluGluArgAsnValCySvPheValProCySvGlyHisValaIaCySv 320  
DB 1106 ATATGTTATTCGAGAGCGCTAACGTGTCTTCGTGCCGTGGCCACGTGGTGGCTGC 1165  
QY 321 AlaIySvCyAlaIeSerThrAspIySvCySvPrometCyAsArgArgThrlPheThrlaAsnAla 340  
DB 1166 GCCAAGTGGCGCCTGTGCGACGAGCAAGTCCCGATGTGTGCGAGAGCGTTCCAGAAATGG 1225  
QY 341 ValArgLeuTyrPheSer 346  
DB 1226 GTGCGGCTCTACTTCTCG 1243  
RESULT 2  
AADI4419  
ID AADI4419 standard; cDNA; 1739 BP.  
XX  
AC AADI4419;  
XX  
DT 01-NOV-2001 (first entry)  
XX  
DE Fall armyworm inhibitor of apoptosis (IAP) cDNA.  
XX  
KW Fall armyworm; inhibitor of apoptosis; IAP; transgenic plant;  
KW apoptosis inhibitor; therapy; acquired immune deficiency syndrome; AIDS;  
KW neurodegenerative disease; Alzheimer's disease; aplastic anaemia;  
KW Parkinson's disease; amyotrophic lateral sclerosis; retinitis pigmentosa;  
KW myelodysplastic syndrome; toxin-induced liver disease; ischaemic injury;  
KW myocardial infarction; stroke; reperfusion injury; cancer; neotropic;  
KW autoimmune disorder; lupus erythematosus; multiple sclerosis; vasotropic;  
KW insecticide; viral infection; anti-HIV; human immunodeficiency virus;  
KW neuroprotective; anti-nausea; cardiant; cerebroprotective; vulnerary;  
KW cytostatic; immunosuppressive; virucide; antialcoholic; se.  
XX  
OS Spodoptera frugiperda.  
XX  
OS  
XX  
FH Key Location/Qualifiers  
FT CDS 229..1362  
FT /tag=a  
FT /product="inhibitor of apoptosis protein"  
FT /note="CDS is referred as SEQ ID NO 2 in the  
FT specification"  
XX  
PN MO200159108-A2.  
XX  
PD 16-AUG-2001.  
XX  
XX 07-FEB-2001; 2001WC-US004071.  
PF  
XX 10-FEB-2000; 2000US-00502528.  
PR  
XX



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OM protein - protein search, using sw model

Run on: November 26, 2005, 16:56:56 ; Search time 86 Seconds  
(without alignments)  
1767.733 Million cell updates/sec

Title: US-10-041-859a-2  
Perfect score: 1887  
Sequence: 1 MELTYKAKKGAATLVMLKN.....TDRCPMCRPTNAVLRYFS 346

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues  
Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_21.\*  
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2: geneseqp1990s:\*  
3: geneseqp2000s:\*  
4: geneseqp2001s:\*  
5: geneseqp2002s:\*  
6: geneseqp2003as:\*  
7: geneseqp2003bs:\*  
8: geneseqp2004s:\*  
9: geneseqp2005s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	% Query Match	Length	ID	Description
1	1887	100.0	346	5	ABBT8046 Amino aci
2	1311	69.5	377	5	AAE07881 Fall army
3	767.5	40.7	263	5	ABB09488 AMLPV bac
4	721.5	38.2	438	4	AAAB48189 Drosophi
5	719.5	38.1	438	4	ABBB61858 Drosophi
6	719.5	38.1	438	4	ABBB67347 Drosophi
7	719.5	38.1	438	4	AAAB48188 Drosophi
8	719.5	38.1	438	4	AAAB48190 Drosophi
9	719.5	38.1	438	8	ADDO08093 fly poly
10	713.5	37.8	438	4	AAAB48192 Drosophi
11	713.5	37.8	438	4	AAAB48191 Drosophi
12	711.5	37.7	438	4	AAAB48196 Drosophi
13	709.5	37.6	438	4	AAAB48197 Drosophi
14	708.5	37.5	438	4	AAAB48193 Drosophi
15	708.5	37.5	438	4	AAAB48194 Drosophi
16	532.5	28.2	434	4	AAAB48195 Drosophi
17	526.5	27.9	604	2	AAWI19747 Human inh
18	526.5	27.9	604	2	AAWI15446 Human c-I
19	526.5	27.9	604	2	AAWI52703 Human cel
20	526.5	27.9	604	6	ABU07431 Protein d
21	526.5	27.9	604	6	ABU07431 Protein d
22	526.5	27.9	604	6	ABU07431 Protein d
23	526.5	27.9	604	7	ABD80948 RING-SH C
24	526.5	27.9	604	7	AAE39811 Human cel

25	526.5	27.9	604	8	ADG87135 Human CIA
26	526.5	27.9	604	8	ADH74643 Human CIA
27	526.5	27.9	604	8	ADG88171 Human pro
28	526.5	27.9	604	8	ADR89114 Human IAP
29	526.5	27.9	604	8	ADR87238 Human bla
30	526.5	27.9	604	8	ADU22899 Human apo
31	525.5	27.8	600	2	AAW69298 Human inh
32	525.5	27.8	600	6	ABP72155 Mouse inh
33	524.5	27.8	604	2	AAWI9582 Human apo
34	524.5	27.8	604	2	AAW69295 Human HIA
35	524.5	27.8	604	5	ABG65664 Human inh
36	517.5	27.4	602	5	ABG65667 Mouse inh
37	516.5	27.4	602	2	AAWI9585 Mouse apo
38	507.5	26.9	618	2	AAWI9583 Human pro
39	507.5	26.9	618	2	AAW69296 Human HIA
40	507.5	26.9	618	5	ABG65665 Human inh
41	501	26.6	497	7	ADI39803 Drosophi
42	500.5	26.5	496	2	AAWI9745 Mouse inh
43	500.5	26.5	618	2	AAWI9746 Human inh
44	500.5	26.5	618	2	AAWI3545 Human c-I
45	500.5	26.5	618	2	AAI33998 Human cel

## ALIGNMENTS

RESULT 1		ABBT8046		standard; protein; 346 AA.	
ID		ABBT8046			
AC		ABBT8046			
DT		22-OCT-2002		(first entry)	
DE		Amino acid sequence of inhibitor of apoptosis protein BmiAP.			
KM		Inhibitor of apoptosis protein; IAP; BmiAP; silkworm; apoptosis; insect;			
XX		Spodoptera frugiperda; insuln-resistant plant; caspase.			
OS		Bombyx mori.			
FH		Key		Location/Qualifiers	
FT		Domain		74..140	
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FT		Domain		182..249	
FT		Domain		/note= "BIR domain 2"	
FT		Domain		298..314	
FT		Domain		/note= "RING domain"	
PN		W0200253586-A2.			
XX		11-JUL-2002.			
XX		07-JAN-2002; 2002WO-US000314.			
XX		08-JAN-2001; 2001US-0260478P.			
XX		(BURN-) BURNHAM INST.			
PA		Maeda S, Huang Q, Reed JC, Devereaux QL;			
XX		WPI; 2002-590628/63.			
DR		N-PSDB; ABO78228.			
XX		Novel recombinant polypeptide, inhibitor of apoptosis protein family			
PT		member BmiAP from silkworm Bombyx mori BmN cells, useful for inhibiting			
PT		apoptosis and identifying an agent that modulates activity of			
XX		polypeptide.			
PS		Claim 39; Page 31; 62pp; English.			
XX		The present score represents a polypeptide which is an inhibitor of			
CC		apoptosis protein (IAP) family member, and designated BmiAP. BmiAP is			

CC derived from silkworm Bombyx mori BmN cells. The BmiAP polypeptide  
CC contains two baculoviral IAP repeat (BIR) domains, followed by a RING  
CC domain. BmiAP polypeptides and polynucleotides are useful for inhibiting  
CC apoptosis in insect cells, especially Spodoptera frugiperda or Bombyx  
CC mori cells, and mammalian cells, and plant cells. They are also useful  
CC for generating a biotic or abiotic insect-resistant plant. BmiAP is also  
CC useful for inhibiting caspases

SQ Sequence 346 AA;

Query Match 100.0%; Score 1887; DB 5; Length 346;  
Best Local Similarity 100.0%; Pred. No. 6, 9e-174;  
Matches 346; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MELTKAKGAATVLMKNARDAKRPFGPLMLSSCESSSTSTLPSPESSADKTDNDH 60  
DB 1 MELTKAKGAATVLMKNARDAKRPFGPLMLSSCESSSTSTLPSPESSADKTDNDH 60  
QY 61 TENFLPDMPMRREERLKTFDQWPVTPLTPEQLANNGFYLLGRGDEVCCAFCKVEIMRW 120  
DB 61 TENFLPDMPMRREERLKTFDQWPVTPLTPEQLANNGFYLLGRGDEVCCAFCKVEIMRW 120  
QY 121 VEGDDPAADHRRAPQCPFVRKQMYANAGGEATAVGRDECGASAAQTQPPMPGPVHARYS 180  
DB 121 VEGDDPAADHRRAPQCPFVRKQMYANAGGEATAVGRDECGASAAQTQPPMPGPVHARYS 180  
QY 181 TEAARLATFKDMPRRMRQKPEELAEAGFFYTGQDGTKCFYCDGGLKDMESDVPWEQHA 240  
DB 181 TEAARLATFKDMPRRMRQKPEELAEAGFFYTGQDGTKCFYCDGGLKDMESDVPWEQHA 240  
QY 241 RWFDRCAVYQVLVGRDYIQKVKSEATPAISASEEQAAATNDSTKNVAOEGEKHLDSKICK 300  
DB 241 RWFDRCAVYQVLVGRDYIQKVKSEATPAISASEEQAAATNDSTKNVAOEGEKHLDSKICK 300  
QY 301 ICSEERNVCFVPCGHVAVACAKALSTDCKPMCRRTFTNAVRLYFS 346  
DB 301 ICSEERNVCFVPCGHVAVACAKALSTDCKPMCRRTFTNAVRLYFS 346

RESULT 2  
AAE07881  
ID AAE07881 standard; protein; 377 AA.

AAE07881;  
01-NOV-2001 (first entry)

DE Fall armyworm inhibitor of apoptosis (IAP) protein.

XX Fall armyworm; inhibitor of apoptosis; IAP; transgenic plant;  
XX apoptosis inhibitor; therapy; acquired immune deficiency syndrome; AIDS;  
XX neurodegenerative disease; Alzheimer's disease; aplastic anaemia;  
XX Parkinson's disease; amyotrophic lateral sclerosis; retinitis pigmentosa;  
XX myelodysplastic syndrome; toxin-induced liver disease; ischaemic injury;  
XX myocardial infarction; stroke; reperfusion injury; cancer; neotropical;  
XX autoimmune disorder; lupus erythematosus; multiple sclerosis; vasculopathy;  
XX insecticide; viral infection; anti-HIV; human immunodeficiency virus;  
XX neuroprotective; antianemic; cardiac; cerebroprotective; vulnerary;  
XX cytoskeletal; immunosuppressive; virucide; antialcoholic.

XX Spodoptera frugiperda.

XX WO200159108-A2.

XX 16-AUG-2001.

XX 07-FEB-2001; 2001WO-US004071.

XX 10-FEB-2000; 2000US-00502528.

XX (REGC ) UNIV CALIFORNIA.  
XX (MAED/) MAEDA H.

PI Maeda S, Hammock BD, Huang Q, Maeda H;  
XX WPI; 2001-514667/56.  
DR N-PSDB; AAD14419.  
XX  
PT Novel nucleic acid construct comprising cDNA encoding inhibitor of  
PT apoptosis proteins, useful for controlling apoptosis in target cells and  
PT for combating various disorders associated with apoptosis.

XX Claim 6; Page 39; 43pp; English.

CC The present sequence is fall armyworm inhibitor of apoptosis (IAP). The  
CC IAP is useful for controlling apoptosis in target cells. It is also  
CC useful for screening compounds that modulate apoptosis and for the  
CC production of transgenic plants. The IAP can be used to delay, suppress  
CC or inhibit an apoptosis response in plants. In animals, IAPs are used to  
CC combat various disorders related to apoptosis, e.g., acquired  
CC immunodeficiency syndrome (AIDS), neurodegenerative diseases (e.g.  
CC Alzheimer's disease, Parkinson's disease, amyotrophic lateral sclerosis),  
CC retinitis pigmentosa and other diseases of retina, myelodysplastic  
CC syndrome (e.g. aplastic anaemia), toxin-induced liver diseases (e.g.  
CC alcoholism), ischaemic injury (e.g. myocardial infarction, stroke and  
CC reperfusion injury), cancers, autoimmune disorders (e.g. lupus  
CC erythematosus and multiple sclerosis) and viral infections. The IAP is  
CC also useful in vitro to monitor the expression of IAP cDNA, and to detect  
CC and monitor the presence of IAPs in a sample. The IAP DNAs are used in  
CC the construction of recombinant baculoviruses that are useful as  
CC insecticides

SQ Sequence 377 AA;

Query Match 69.5%; Score 1311; DB 4; Length 377;  
Best Local Similarity 68.5%; Pred. No. 5, 5e-118;  
Matches 248; Conservative 39; Mismatches 57; Indels 18; Gaps 7;

QY 1 MELTKAKGAATVLMKN-ARDAKMRPFGPLML--SSCESSSTSTLPSPESS----- 51  
DB 18 MDITKVASNGSSSTLTLLFRKSGLEAKIRP-LAPLMLPTPSYDSNMGSPSLSPSTPCSSSS 76  
QY 52 -SADKTDNHDFTFNFLPDMPMRREERLKTFDQWPVTPLTPEQLANNGFYLLGRGDEVCC 110  
DB 77 FSIDKTDNHDFTFGFSADYDVMKKEDEMRKTFEKMPSFISGQLARNGFYLLGRBREAC 136  
QY 111 AFCKVEIMRWVEGDDPAADHRRAPQCPFVRKQMYANAGGEATAVGRDECGASAA--TQ 167  
DB 137 AFCKVEIMRWVEGDDPAADHRRAPQCPFVRK-LNGTAADPSSSGQDCGARAAPSGTS 195  
QY 168 PRMPGPVHARYSTEARLATFKDMPRRMRQKPEELAEAGFFYTGQDGTKCFYCDGGLK 227  
DB 196 PRMPGPVHARYSTEARLARLSFKDMPRCMRQKPEELAEAGFFYTGQDGTKCFYCDGGLK 255  
QY 228 DMESDVPWEQHAARMWDRCAVYQVLVGRDYIQKVKSEATPAISASEEQ--AATNDSTKN 284  
DB 256 DMENHDVPWEQHAARMWDRCAVYQVLVGRDYIQKVKSEATPAISASEEQ--AATNDSTKN 315  
QY 285 VAOEGEKHLDSKICKICYSEERNVCFVPCGHVAVACAKALSTDCKPMCRRTFTNAVRLY 344  
DB 316 PAEAPENSVDGSLCKTCYAEERNVCFVPCGHVAVACAKALADCKPMCRRTFTNAVRLY 375  
QY 345 FS 346  
DB 376 FS 377

RESULT 3  
ABB09488  
ID ABB09488 standard; protein; 263 AA.

ABB09488;

XX 01-JUL-2002 (first entry)  
XX AMEPV baculovirus-like inhibitor of apoptosis (AMV133).

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 26, 2005, 17:25:31 ; Search time 109 Seconds  
(without alignments)  
2239.567 Million cell updates/sec

Title: US-10-041-859A-2  
Perfect score: 1887  
Sequence: 1 MELTKVAKNGAATLVMLKN.....TDKPCMCRTFTNAVLVYFS 346

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database : UniProt 05.80.\*  
1: uniprot\_sprot.\*  
2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1887	100.0	346	Q968T8_BOMMO	Q968T8 bombyx mori
2	1866	98.9	346	Q81S31_BOMMO	Q81S31 bombyx mori
3	1327	70.3	379	Q9U482_TRINI	Q9U482 trichoplusi
4	1311	69.5	377	Q9NU07_SPOFR	Q9NU07 spodoptera
5	966	51.2	275	IAP_GVCP	IAP1436 cydia pomon
6	937	49.7	287	Q6E7G7_NPVAG	Q6E7G7 anticarsia
7	890.5	47.2	280	Q6VTV9_NPVCD	Q6VTV9 choristoneu
8	879	46.6	263	Q80SF4_NPVHC	Q80SF4 hyphantia
9	876	46.4	281	Q9YXN8_NPVCF	Q9YXN8 choristoneu
10	873	46.3	261	Q9QES9_NPVCF	Q9QES9 epiphyas po
11	873	46.3	276	Q89744_NPVBS	Q89744 buzura supp
12	862	45.7	268	IAP3_NPVOP	P41437 oryzaia psen
13	782	41.4	264	Q9EN37_AMEPV	Q9EN37 amsacta moo
14	747.5	39.6	255	Q7TS81_GVCL	Q7TS81 cypripodoleb
15	728	38.6	313	Q9J827_9NUCL	Q9J827 spodoptera
16	719.5	38.1	438	IAP1_DROME	Q24306 drosophila
17	701	37.1	403	Q8WRD9_AEDTR	Q8WRD9 aedes trise
18	684	36.2	401	Q6Q507_ABDAL	Q6Q507 aedes aegypt
19	676.5	35.9	402	Q8T621_ABDAL	Q8T621 aedes albop
20	662	35.1	285	Q8JMI6_9NUCL	Q8JMI6 mamestra co
21	653	34.6	276	Q71A73_9NUCL	Q71A73 mamestra co
22	653	34.6	276	Q8QJ95_NPVHC	Q8QJ95 mamestra co
23	635	33.7	283	Q80LX8_NPVAR	Q80LX8 adoxophyes
24	623.5	33.0	278	Q4KT41_9NUCL	Q4KT41 chrysodeixi
25	573	30.4	254	Q7T966_GVAVO	Q7T966 adoxophyes
26	550	29.1	414	Q4T660_TETNG	Q4T660 tetraodon n
27	544.5	28.9	269	Q6QXJ6_GVAVS	Q6QXJ6 agrotis seg
28	542	28.7	358	IAP_PIG	Q6Z640 sus scrofa
29	538.5	28.5	304	Q5TWG6_ANOGA	Q5TWG6 anopheles g
30	532.5	28.2	268	Q9E232_9NUCL	Q9E232 helioverpa
31	530.5	28.1	401	Q8JHV9_XENLA	Q8JHV9 xenopus lae

32	530	28.1	186	2	Q7QJ55_ANOGA	Q7QJ55 anopheles g
33	529.5	28.1	268	2	Q77LM6_9NUCL	Q77LM6 helioverpa
34	529.5	28.1	268	2	Q91F18_9NUCL	Q91F18 helioverpa
35	528.5	28.0	602	2	Q9ESE9_RAT	Q9ESE9 rattus norv
36	526.5	27.9	602	2	Q5X1W4_RAT	Q5X1W4 rattus norv
37	526.5	27.9	604	1	BIRC3_HUMAN	Q13489 homo sapien
38	525.5	27.8	600	1	BIRC3_MOUSE	Q08863 mus musculu
39	520.5	27.6	604	2	Q6DDV3_XENLA	Q6DDV3 xenopus lae
40	516.5	27.4	616	2	Q804E2_ICRPU	Q804E2 ictalurus p
41	513.5	27.2	604	2	Q6GUD7_XENR	Q6GUD7 xenopus tro
42	513	27.2	628	2	Q8WMD2_BRARE	Q8WMD2 brachydanio
43	513	27.2	647	2	Q7T0K2_BRARE	Q7T0K2 brachydanio
44	513	27.2	654	2	Q6ZM93_BRARE	Q6ZM93 brachydanio
45	511.5	27.1	639	2	Q4SFS0_TETNG	Q4SFS0 tetraodon n

## ALIGNMENTS

RESULT 1						
ID	Q968T8_BOMMO	PRELIMINARY;	PRT;	346	AA.	
AC	Q968T8;					
DT	01-DEC-2001 (TREMBLrel. 19, Created)					
DT	01-DEC-2001 (TREMBLrel. 19, Last sequence update)					
DT	01-JUN-2003 (TREMBLrel. 24, Last annotation update)					
DE	Inhibitor of apoptosis protein.					
GN	Name-IAP;					
OS	Bombyx mori (Silk moth).					
OC	Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;					
OC	Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Bombycoidea;					
OC	Bombycidae; Bombyx.					
OX	NCBI_Taxid=7091;					
RN	[1]					
RP	NOCTECTIDE SEQUENCE.					
RX	MEDLINE=21240184; PubMed=11341966; DOI=10.1016/S0167-4889(00)00105-1;					
RA	Huang Q., Devereux Q.L., Maeda S., Stennicke H.R., Hammock B.D.,					
RA	Reed J.C.;					
RT	"Cloning and characterization of an inhibitor of apoptosis protein					
RT	(IAP) from Bombyx mori.";					
RL	Biochim. Biophys. Acta 1499:191-198(2001).					
DR	EMBL; AF281073; AAK57560.1; -, mRNA.					
DR	HSSP; Q24306; 1Q4Q.					
DR	GO; GO:00000151; C:ubiquitin ligase complex; IEA.					
DR	GO; GO:0004842; F:ubiquitin-protein ligase activity; IEA.					
DR	GO; GO:0008270; F:zinc ion binding; IEA.					
DR	GO; GO:0016567; P:anti-apoptosis; IEA.					
DR	InterPro; IPR001370; Prot inh 132_IAP.					
DR	InterPro; IPR001841; Znf_Fing-					
DR	Pfam; PF00653; BIR_2.					
DR	SMART; SM00238; BIR_2.					
DR	SMART; SM00184; BIR_1.					
DR	PROSITE; PS01282; RING_REPEAT_1; 2.					
DR	PROSITE; PSS0143; BIR_REPEAT_2; 2.					
DR	PROSITE; PSS0089; ZF_RING_2; 1.					
DR	SEQUENCE 346 AA; 38942 MW; 6CFCC6468894C69 CRC64;					
Query Match						
Best Local Similarity 100.0%; Score 1887; DB 2; Length 346;						
Matches 346; Conservative 0; Mismatches 0; Indels 0; Gaps 0;						
QY	1	MELTKVAKNGAATLVMLKNARDAKMPFTGPTMLSSCESSTSTLPSSSSADKTNHD	60			
DB	1	MELTKVAKNGAATLVMLKNARDAKMPFTGPTMLSSCESSTSTLPSSSSADKTNHD	60			
QY	61	TFNFLPMPMRREERELKTFDQMPVTLTPEOLARNGFYLLRGDGVCCAFCKVEIMRW	120			
DB	61	TFNFLPMPMRREERELKTFDQMPVTLTPEOLARNGFYLLRGDGVCCAFCKVEIMRW	120			
QY	121	VEGDPPAADHRRWAPQCPFYRKQNTYANAGEATVAGRDGASANTPPMPGPVHARYS	180			
DB	121	VEGDPPAADHRRWAPQCPFYRKQNTYANAGEATVAGRDGASANTPPMPGPVHARYS	180			

QY 181 TEAARLATPKDWRMRMRKQKEBELAEAGFFYTGGDKTKCFYCDGGLKDWESDDVPWEQHA 240  
DB 181 TEAARLATPKDWRMRMRKQKEBELAEAGFFYTGGDKTKCFYCDGGLKDWESDDVPWEQHA 240  
QY 241 RWFDRCAVYQVLVNGRDYIQVKSEBATAISASEEQAAATNDSTKNVAOEGEKHLDDSKICK 300  
DB 241 RWFDRCAVYQVLVNGRDYIQVKSEBATAISASEEQAAATNDSTKNVAOEGEKHLDDSKICK 300  
QY 301 ICYSEERNVCFVPCGHVAVACAKALSTDCKPCMCRRFTTNAVRLYFS 346  
DB 301 ICYSEERNVCFVPCGHVAVACAKALSTDCKPCMCRRFTTNAVRLYFS 346

RESULT 2  
081S31\_BOMMO PRELIMINARY; PRT; 346 AA.  
ID 081S31\_BOMMO PRELIMINARY; PRT; 346 AA.  
AC 081S31; 23, Created)  
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE Inhibitor of apoptosis protein.  
OS Bombyx mori (Silk moth).  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditylata; Bombycoidea;  
OC Bombycidae; Bombyx.  
NCBI\_TaxID=7091;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RA Yang G., Wang L., Wu X.,  
RL Submitted (Sep-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AY155274; AAN46650.1; -, mRNA.  
DR HSSP; Q24306; 104Q.  
DR GO; GO:0000151; C:ubiquitin ligase complex; IEA.  
DR GO; GO:0004842; F:ubiquitin-protein ligase activity; IEA.  
DR GO; GO:0008270; F:zinc ion binding; IEA.  
DR GO; GO:0006916; P:anti-apoptosis; IEA.  
DR GO; GO:0016567; P:protein ubiquitination; IEA.  
DR InterPro; IPR001370; ProC\_inh\_132\_IAP.  
DR InterPro; IPR001841; Znf\_Ring.  
DR Pfam; PF00653; BIR; 2.  
DR SMART; SM00238; BIR; 2.  
DR SMART; SM00184; RING; 1.  
DR PROSITE; PS01282; BIR\_REPEAT\_1; 2.  
DR PROSITE; PS50143; BIR\_REPEAT\_2; 2.  
DR PROSITE; PS50089; ZF\_RING\_2; 1.  
SQ SEQUENCE 346 AA; 38849 MW; 5450EB75F56A846 CRC64;

Query Match 98.9%; Score 1866; DB 2; Length 346;  
Best Local Similarity 99.1%; Pred. No. 8.6e-143;  
Matches 343; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 1 MELTKVAKNGAATLVMLKNARDAKMRPFIGPLMLSSCESSSTSTLPSRSSADKTDNDH 60  
DB 1 MELTKVAKNGAATLVMLKNARDAKMRPFIGPLMLSSCESSSTSTLPSRSSADKTDNDH 60  
QY 61 TTFNLPDMPMRREBERLKTFDQMPVTLTPEQLARNGFYLLGRGDEVCAFCVKEIMRW 120  
DB 61 TTFNLPDMPMRREBERLKTFDQMPVTLTPEQLARNGFYLLGRGDEVCAFCVKEIMRW 120  
QY 121 VEGDDPAADHRRNAPQCFPRKQMYANAGBATAVGRDECGASANTOPPMGPVTHARYS 180  
DB 121 VEGDDPAADHRRNAPQCFPRKQMYANAGBATAVGRDECGASANTOPPMGPVTHARYS 180  
QY 181 TEAARLATPKDWRMRMRKQKEBELAEAGFFYTGGDKTKCFYCDGGLKDWESDDVPWEQHA 240  
DB 181 TEAARLATPKDWRMRMRKQKEBELAEAGFFYTGGDKTKCFYCDGGLKDWESDDVPWEQHA 240  
QY 241 RWFDRCAVYQVLVNGRDYIQVKSEBATAISASEEQAAATNDSTKNVAOEGEKHLDDSKICK 300  
DB 241 RWFDRCAVYQVLVNGRDYIQVKSEBATAISASEEQAAATNDSTKNVAOEGEKHLDDSKICK 300  
QY 301 ICYSEERNVCFVPCGHVAVACAKALSTDCKPCMCRRFTTNAVRLYFS 346  
DB 301 ICYSEERNVCFVPCGHVAVACAKALSTDCKPCMCRRFTTNAVRLYFS 346

DB 301 ICYSEERNVCFVPCGHVAVACAKALSTDCKPCMCRRFTTNAVRLYFS 346

RESULT 3  
09U492\_TRINI PRELIMINARY; PRT; 379 AA.  
ID 09U492\_TRINI PRELIMINARY; PRT; 379 AA.  
AC 09U492; 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Inhibitor of apoptosis protein.  
GN Name=IAP1;  
OS Trichoplusia ni (Cabbage looper).  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditylata; Noctuoidea;  
OC Noctuidae; Plutellinae; Trichoplusia.  
NCBI\_TaxID=7111;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RA MEDLINE=20062908; PubMed=10593985; DOI=10.1074/jbc.274.51.36769;  
RX Sesahgiri S., Vucic D., Lee J., Dixit V.M.;  
RT "Baculovirus-based genetic screen for antiapoptotic genes identifies a novel IAP".  
RT J. Biol. Chem. 274:36769-36773(1999).  
DR EMBL; AF195528; AAF19819.1; -, mRNA.  
DR HSSP; Q24306; 104Q.  
DR GO; GO:0000151; C:ubiquitin ligase complex; IEA.  
DR GO; GO:0004842; F:ubiquitin-protein ligase activity; IEA.  
DR GO; GO:0008270; F:zinc ion binding; IEA.  
DR GO; GO:0006916; P:anti-apoptosis; IEA.  
DR GO; GO:0016567; P:protein ubiquitination; IEA.  
DR InterPro; IPR001370; ProC\_inh\_132\_IAP.  
DR InterPro; IPR001841; Znf\_Ring.  
DR Pfam; PF00653; BIR; 2.  
DR SMART; SM00238; BIR; 2.  
DR SMART; SM00184; RING; 1.  
DR PROSITE; PS01282; BIR\_REPEAT\_1; 2.  
DR PROSITE; PS50143; BIR\_REPEAT\_2; 2.  
DR PROSITE; PS50089; ZF\_RING\_2; 1.  
SQ SEQUENCE 379 AA; 41857 MW; 069381A012D9D65 CRC64;

Query Match 70.3%; Score 1327; DB 2; Length 379;  
Best Local Similarity 69.0%; Pred. No. 4.5e-99;  
Matches 251; Conservative 39; Mismatches 54; Indels 20; Gaps 8;  
QY 1 MELTKVAKNGAATLVMLKNA-RDAKMRPFIGPLML--SSCESSSTSTLPSRSS----- 51  
DB 18 MDITTKVANSNGPASPFLTFKNAAPDAKIRPLV-PLVLPQTQSYDSNAGSPASSFSTPSSSS 76  
QY 52 -SADKTDNDHTDNFLLPDMEMRREBERLKTFDQMPVTLTPEQLARNGFYLLGRGDEVCC 110  
DB 77 FSDIKTDNDHTSLTADAVDMSREDERIKTFEKMPVPSFLSGQLARNGFYLLGRGDEVCC 136  
QY 111 AFCKVEIMRWVSGDDPAADHRRNAPQCFPRKQMYANAGBATAVGRDECGASAA--TOP 168  
DB 137 AFCKVEIMRWVSGDDPAADHRRNAPQCFPRK-LGGGVNTDSGAAGRDECGAARAAFTSSP 195  
QY 169 PRMPGPVTHARYSSEAARLATPKDWRMRMRKQKEBELAEAGFFYTGGDKTKCFYCDGGLD 228  
DB 196 SRMPGPVTHARYSSEAARLATPKDWRMRMRKQKEBELAEAGFFYTGGDKTKCFYCDGGLD 255  
QY 229 WESDDVPWEQHAHWPDRCAVYQVLVNGRDYIQVKSEBATAI---SASEEB---QAAATNDST 282  
DB 256 WENDVDVPWEQHAHWPDRCAVYQVLVNGREYQVKMTACIIPAPAPRDPAPASAAPEPV 315  
QY 283 KNAOEGEKHLDDSKICKI CYSEERNVCFVPCGHVAVACAKALSTDCKPCMCRRFTTNAVR 342  
DB 316 VSAABEQESTLSDSKICKI CFAEERNVCFVPCGHVAVACAKALAADCKPCMCRRFTTNAVR 375  
QY 343 LYFS 346  
DB 376 LYFS 379

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: November 26, 2005, 00:14:08 ; Search time 18362 Seconds  
(without alignments)  
11680.119 Million cell updates/sec

Title: US-10-041-859A-1

Sequence: 1 cactatcaactcactctcac.....tgcgcctcactctctgtga 3773

Scoring table: IDENTITY NUC  
Gapop 10.0, Gapext 1.0

Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

- 1: gb\_ba:\*
- 2: gb\_in:\*
- 3: gb\_env:\*
- 4: gb\_om:\*
- 5: gb\_ov:\*
- 6: gb\_pat:\*
- 7: gb\_ph:\*
- 8: gb\_pr:\*
- 9: gb\_ro:\*
- 10: gb\_sta:\*
- 11: gb\_sy:\*
- 12: gb\_un:\*
- 13: gb\_vl:\*
- 14: gb\_hlg:\*
- 15: gb\_pl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3773	100.0	3773	6	AX664311 Sequence
2	2716	72.0	2716	2	AF281073 Bombyx mo
3	1033	27.4	1041	2	AY155274 Bombyx mo
4	441.8	11.7	1739	2	AF186378 Spodopter
5	441.8	11.7	1739	6	AR340174 Sequence
6	441.8	11.6	1134	6	AX213188 Sequence
7	437.2	11.6	1134	6	AR340175 Sequence
8	437.2	11.5	2614	2	AF213189 Sequence
9	433.8	11.5	2614	2	AF195528 Trichoplu
10	292.8	7.2	123500	13	US3466 Cydia pomon
11	270	7.2	1247	13	AY525121 Anticarsa
12	254	6.7	1032	13	CFU82510 Choristoneu
13	254	6.7	129593	13	AF512031 Choristoneu
14	226.6	6.0	131995	13	OPU75930 Oryzia pseu
15	226.2	6.0	3248	13	AF045936 Buzura su
16	218.6	5.8	131160	13	AY327402 Choristoneu
17	218.6	5.5	1241	13	AB088850 Hyphantri
18	208.2				

C 19	200.6	5.3	1787	13	AF180757 Epiphyas
C 20	200.6	5.3	118584	13	AY043265 Epiphyas
C 21	161	4.3	110907	13	AY229887 Cyrtophyl
C 22	142.4	3.8	50000	6	AX392733 Sequence
C 23	142.4	3.8	232392	13	AF250284 Amsacta m
C 24	130.4	3.5	17394	6	AX382714 Sequence
C 25	130	3.4	113220	13	AP006270 Adoxophye
C 26	120.6	3.2	135611	13	AF169823 Spodopter
C 27	117	3.1	134394	13	DQ017380 Trichoplu
C 28	115	3.0	158482	13	AY126275 Mamestra
C 29	113.6	3.0	256	2	AY751528 Spodopter
C 30	112.4	3.0	133877	14	AC120883 Homo sapi
C 31	111.8	3.0	8056	6	AX599046 Sequence
C 32	110.8	2.9	67970	2	PFMAL1P3 AL031746 Plasmodiu
C 33	109.8	2.9	8056	6	AX599046 Sequence
C 34	109.8	2.9	313050	2	PFAL29352 AL929352 Plasmodiu
C 35	109.6	2.9	178193	14	CR392006 Danio rer
C 36	109.2	2.9	258658	2	AE014832 Plasmodiu
C 37	109	2.9	135121	8	AC069525 Homo sapi
C 38	108.2	2.9	348174	2	CR382399 Plasmodiu
C 39	108	2.8	67970	2	PFMAL1P3 AL031746 Plasmodiu
C 40	107.2	2.8	110000	14	TANNA.01 Continuation (2 of
C 41	107	2.8	86826	2	PFMAL3F5 AL034556 Plasmodiu
C 42	106.4	2.8	4601	2	DMU11584 U11584 Drosophila
C 43	106.4	2.8	19517	2	DMU17541 U37541 Drosophila
C 44	106.2	2.8	1662	2	AF447592 Ochlerota
C 45	105.8	2.8	254050	2	PFAL29358 Plasmodiu

ALIGNMENTS

RESULT 1	AX664311	3773 bp	DNA	linear	PAT 22-MAR-2003
LOCUS	AX664311				
DEFINITION	Sequence 1 from Patent WO02053586.				
ACCESSION	AX664311				
VERSION	AX664311.1	GI:29164241			
KEYWORDS					
SOURCE	Bombyx mori (domestic silkworm)				
ORGANISM	Bombyx mori				
REFERENCE	1				
AUTHORS	Huang, Q., Reed, J.C., Devereaux, Q.L. and Maeda, S.D.				
TITLE	Inhibitor of apoptosis proteins and nucleic acids and methods for making and using them				
JOURNAL	Patent: WO 02053586-A 1 11-JUL-2002;				
FEATURES	The Burnham Institute (US)				
source	location/Qualifiers				
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ORIGIN

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GenCore version 5.1.6  
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

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2	1887	100.0	3773	6 AX664311	Sequence
3	1866	98.9	1041	2 AY155274	Bombyx mo

4	1327	70.3	2614	2 AF195528	AF195528 Trichoplin
5	1311	69.5	1134	6 AR340175	AR340175 Sequence
6	1311	69.5	1134	6 AX213189	AX213189 Sequence
7	1311	69.5	1739	2 AF163378	AF163378 Spodopter
8	1311	69.5	1739	6 AR340174	AR340174 Sequence
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10	966	51.2	123500	13 U53466	U53466 Cydia pomon
11	937	49.7	1247	13 AY525121	AY525121 Anticarsa
12	890.5	47.2	131160	13 AY327402	AY327402 Choriston
13	884	46.8	129593	13 AF512031	AF512031 Choriston
14	879	46.6	1241	13 AB088850	AB088850 Hyphantri
15	876	46.4	1032	13 CF082510	CF082510 Choristoneu
16	873	46.3	1787	13 AF180757	AF180757 Epiphyas
17	873	46.3	3248	13 AF045936	AF045936 Buzura su
18	873	46.3	118584	13 AY043265	AY043265 Epiphyas
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21	787	41.7	50000	6 AX392733	AX392733 Sequence
22	787	41.7	232392	13 AF250284	AF250284 Ambacta m
23	748	39.6	794	6 AX392714	AX392714 Sequence
24	747.5	39.6	110907	13 AY229987	AY229987 Cryptophl
25	728	38.6	135611	13 AF169823	AF169823 Spodopter
26	725.5	38.4	1317	6 AR432086	AR432086 Sequence
27	723.5	38.3	1317	6 AR432085	AR432085 Sequence
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36	719.5	38.1	176056	2 AC010066	AC010066 Drosophila
37	719.5	38.1	283815	2 AE003528	AE003528 Drosophila
38	717.5	38.0	1317	6 AR432088	AR432088 Sequence
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44	712	37.7	1662	2 AF447592	AF447592 Ochlerota
45	707	37.5	1484	2 AY119524	AY119524 Drosophila

## ALIGNMENTS

RESULT 1	AF281073	2716 bp	mrna	linear	INV 30-MAY-2001
LOCUS	Bombyx mori inhibitor of apoptosis protein (IAP) mRNA, complete cds.				
DEFINITION	AF281073.1 GI:14248545				
ACCESSION	AF281073				
VERSION	AF281073.1				
KEYWORDS	Bombyx mori (domestic silkworm)				
SOURCE	Bombyx mori				
ORGANISM	Bombyx mori				
REFERENCE	Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Bombycoidea; Bombycidae; Bombyx.				
AUTHORS	1 (bases 1 to 2716) Huang,Q., Devereaux,Q.L., Maeda,S., Stennicke,H.R., Hammock,B.D. and Reed,J.C.				
TITLE	Cloning and characterization of an inhibitor of apoptosis protein (IAP) from Bombyx mori				
JOURNAL	Biochim. Biophys. Acta 1499 (3), 191-198 (2001)				
PUBMED	11341966				
REFERENCES	2 (bases 1 to 2716) Huang,Q., Devereaux,Q.L., Maeda,S., Salvesen,G.S., Stennicke,H.R., Hammock,B.D. and Reed,J.C.				
AUTHORS	Submitted (21-JUN-2000) Entomology, University of California at Davis, One Shields Avenue, Davis, CA 95616, USA				
TITLE	Location/Qualifiers				
JOURNAL					
FEATURES					

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## ORIGIN

## Alignment Scores:

Pred. No.: 1 37e-126 Length: 2716  
Score: 1887.00 Matches: 346  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 2 Gaps: 0

US-10-041-859A-2 (1-346) x AF281073 (1-2716)

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## RESULT 2

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LOCUS Sequence 1 from Patent WO02053586.  
DEFINITION AX664311  
ACCESSION AX664311  
VERSION AX664311.1 GI:29164241  
KEYWORDS  
SOURCE Bombyx mori (domestic silkworm)  
ORGANISM Bombyx mori  
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;  
Bombycoidea; Bombycidae; Bombyx.

REFERENCE 1  
Huang, Q., Reed, J. C., Devereaux, Q. L. and Maeda, S. D.  
Inhibitor of apoptosis proteins and nucleic acids and methods for  
making and using them  
Patent: WO 02053586-A 1 11-JUN-2002;  
JOURNAL The Burnham Institute (US)  
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Location/Qualifiers

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CFYCDGGLDWESDVPMEOHARWPRCAVYOLVGRDYIOVKSEBATAISASEEOA  
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RTFTNAVRLYFS"

## ORIGIN

## Alignment Scores:

Pred. No.: 2.01e-126 Length: 3773  
Score: 1887.00 Matches: 346  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0



DB: 6 Gaps: 0  
US-10-041-859A-2 (1-346) x AX664311 (1-3773)  
QY 1 MetGluLeuThrIysValAlaIysAsnGlyAlaAlaThrLeuValMetLeuLysAsn 20  
DB 206 ATGAGAGTTGACGAAAGTGTCTAAATAATGAGAGCTGCCCGCAGTTGGATGTTAAAAAT 265  
QY 21 AlaArgAspAlaIysMetArgProPheIleGlyProLeuMetLeuSerSerCysGluSer 40  
DB 266 GCCCGGGATCCAAATAATGCAACCTTTCATTTGTCCTGCTCAATGTTATCTCTGCTGTAATCT 325  
QY 41 SerThrThrSerThrLeuProSerProSerSerSerAlaAspLysThrAspAsnHisAsp 60  
DB 326 TCACAGCATCCACACTCCCGTCACTTTCGTGCTGCTGATTAACGATTAATCAAGAC 385  
QY 61 ThrPheAsnPheLeuProAspMetProAspMetArgArgGluGluGluValGluLeuLysThr 80  
DB 386 ACATTCMACTCTCTCTGATATGCGCAGACATGCTGTGTAAGAGAACCTCTGAAAAACA 445  
QY 81 PheAsnGluThrProValThrPheLeuThrProGluGluLeuAlaArgAsnGlyPheThr 100  
DB 446 TTTCATCAGTGGCCCGCTTACGTTTGTGACCCGGAACAAATGGCCGCAACGATTTCTAC 505  
QY 101 TyrLeuGlyArgGlyAspGluValCysCysAlaPheCysLysValGluIleMetArgTrp 120  
DB 506 TACCTCGGTGGCGGCGACGAAAGTGTCTGTCTTCTGTAAGTAAATTAATGAGGTGG 565  
QY 121 ValGluGlyAspAspProAlaAlaAspHisArgArgTrpAlaProGlnCysProPheVal 140  
DB 566 GTGGAAGGCCACATCTCTGCGCGCATCTGAGATGGCGCGCCCGCATGTCTCTTGTGA 625  
QY 141 ArgLysGluMetTyrIleAsnAlaGlyGlyGluAlaThrAlaValGlyArgAspGluCys 160  
DB 626 CGAAACAAATGATGTCACACGCTGGGGAGAGCGACCCCTGTCTGTAAGAGCAATGT 685  
QY 161 GlyAlaSerAlaAlaThrGlnProProArgMetProGlyProValHisAlaArgTyrSer 180  
DB 686 GGGGCGAGTGGCGGCGACGAGCTCTCCCGATGCGCGGCCCGCGACGCGGTAATCTCC 745  
QY 181 ThrGluAlaAlaArgLeuAlaThrPheLysAspTrpProArgMetArgGlnLysPro 200  
DB 746 ACCGAGGCGCGCGGCTCGCCACCTTCAGAGACTGGCGAGACGTATGCCCAAAAAACC 805  
QY 201 GluGluLeuAlaGluAlaGlyPhePheThrGlyGluGluLysAspLysThrLysCysPhe 220  
DB 806 GAGGAACCTGGCAGAGCGGAGTCTTCTATACAGGCGCAAGGTGACAAACGAAATGCTTC 865  
QY 221 TyrCysAspGlyGlyLeuLysAspTrpGlySerAspAspValProTrpGluGlnHisAla 240  
DB 866 TATTTGCGACCGAGGGCTTAATAAGATTGGGAAAGCATGACTTCCGTGGAAACGACAGCC 925  
QY 241 ArgTrpPheAspArgCysAlaIleTyrValGluLeuValLysGlyArgAspTyrIleGlnLys 260  
DB 926 AGATGAGTTCCAGCGCTCGCGGTACGTCAATGGTGAAGACGTGACTACATTCAGAG 985  
QY 261 ValLysSerGluAlaThrAlaIleSerAlaSerGluGluGluGlnAlaAlaThrAsnAsp 280  
DB 986 GTAAAGTCGAGGCGCATGCGATATCTGTACGAAACAAACAGGCGCGCACCAATGAT 1045  
QY 281 SerThrLysAsnValAlaGlnGluGlyGlyIleHisLeuAspAspSerLysIleCysLys 300  
DB 1046 TCACATCAAGAACGTCCGCCCAAGAGGCGGAGAAACATTGGATGACTTAATAATATGTA 1105  
QY 301 IleCysTyrSerGluGluArgAsnValCysPheValProCysGlyHisValAlaIleCys 320  
DB 1106 ATATGTAATCCGAGAGCGTAAAGTGTGCTGCGCGCGCACGATGTGGCGCTGC 1165  
QY 321 AlaLysCysAlaLeuSerThrAspLysCysProMetCysArgArgTrpPheThrAsnAla 340  
DB 1166 GCCAAGTGGCGCGCTGACGAGCAAGTGCCTCCAGTGTGCGAGAGACGTTCAAGATGG 1225  
QY 341 ValArgLeuTyrPheSer 346

DB 1226 GTGCGGCTCTACTTCTCG 1243  
RESULT 3  
AY155274 1041 bp mRNA linear INV 23-OCT-2002  
LOCUS  
DEFINITION  
Bombyx mori inhibitor of apoptosis protein mRNA, complete cds.  
AY155274  
VERSION  
AY155274.1 GI:24286570  
KEYWORDS  
Bombyx mori (domestic silkworm)  
SOURCE  
Bombyx mori  
ORGANISM  
Bombyx mori  
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;  
Bombycoidea; Bombycidae; Bombyx.  
REFERENCE  
1 (bases 1 to 1041)  
Yang, G., Wang, L., and Wu, X.  
A novel isoform of inhibitor of apoptosis from lepidoptera Bombyx mori (BmIAPv)  
Unpublished  
JOURNAL  
2 (bases 1 to 1041)  
Yang, G., Wang, L., and Wu, X.  
Direct Submission  
AUTHORS  
Submitted (25-SEP-2002) Functional Gene and Biotechnology, Shanghai  
Biochemistry and Cell Biology Chinese Academy of Sciences, 320  
Yue-Yang road, Shanghai 200031, People's Republic of China  
location/Qualifiers  
FEATURES  
source  
1..1041  
/organism="Bombyx mori"  
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GASATQPSRMPEPVHARYSTEARATATPKDMPKROKREBELABGFYTGQGDTK  
CFYCDGLKDWSEDDVPMEOHARWMPRCAYVVLVKRDYIOKYSRATAIASEREOA  
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ORIGIN  
Alignment Scores:  
Pred. No.: 1,47e-125 Length: 1041  
Score: 1866.00 Matches: 343  
Percent Similarity: 99.13% Conservative: 0  
Best Local Similarity: 99.13% Mismatches: 3  
Query Match: 98.89% Indels: 0  
DB: 2 Gaps: 0  
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QY 1 MetGluLeuThrIysValAlaIysAsnGlyAlaAlaThrLeuValMetLeuLysAsn 20  
DB 1 ATGAGAGTTGACGAAAGTGTCTAAATAATGAGAGCTGCCCGCAGTTGGATGTTAAAAAT 60  
QY 21 AlaArgAspAlaIysMetArgProPheIleGlyProLeuMetLeuSerSerCysGluSer 40  
DB 61 GCCCGGGATCCAAATAATGCAACCTTTCATTTGTCCTGCTCAATGTTATCTCTGCTGTAATCT 120  
QY 41 SerThrThrSerThrLeuProSerProSerSerSerAlaAspLysThrAspAsnHisAsp 60  
DB 121 TCACAGCATCCACACTCCCGTCACTTTCGTGCTGCTGATTAACGATTAATCAAGAC 180  
QY 61 ThrPheAsnPheLeuProAspMetProAspMetArgArgGluGluGluValGluLeuLysThr 80

Db 181 ACATTCACCTTCCTCTGTATATGCCGACATGCGTGGAGAGACGCTGTAAAAACA 240  
Qy 81 PheAPSGINTPProValThrPheLeuThrProGluGluLeuAlaArgAnGIyPheYr 100  
Db 241 TTTGATCACTGCGCCCTTACGTTTGTAGCCCGGAAACATTTGGCCCGCAACGATTTCTAC 300  
Qy 101 TTTLeuGluYArgGluYArgGluValCysCysAlaPheCysAlaValGluIleMetArgTTP 120  
Db 301 TACCTCGGTGCGCGGACGAGAGTGTCTGTGCTTTCTGTAGGTAGAAATTATGAGGTGG 360  
Qy 121 ValGluGluYAspAspProAlaAlaAspHisArgArgTTPAlaProGlnCysProPheVal 140  
Db 361 GTCGAAGGCGACGATCTCTGCGCGGATCATCGGAGATGGCGGCCCAAGTCTCTTTGTA 420  
Qy 141 ArgLYeGImeTyrAlaAsnAlaGluYGLuAlaThrAlaValGluYArgAspGluCys 160  
Db 421 CGAAAACAAATGATGTCACACCTGGGGGAGAGGCGCGCTTCGGTGAAGACGAAATGT 480  
Qy 161 GLYAlaSerAlaAlaThrGlnProProArgMetProGluYProValHisAlaArgYrSer 180  
Db 481 GGGGCGAGTGGCGGACGACGAGCTTCCCGCATGCGCGGCCCGCGTGCACGCGCGTACTCC 540  
Qy 181 ThrGluAlaAlaArgGluAlaThrPheLYeAspTTPProArgArgMetArgGlnLYePro 200  
Db 541 ACCGAGGCGCGCGCGCTCGCACCTTTCAGAGACTGGCGCGGATGTATGGCCAAAAACCC 600  
Qy 201 GLuGluLeuAlaGluYArgGluPhePheYrThrGluYGLuGluYAspLYeThrLYeCysPhe 220  
Db 601 GAGGAACCTGGCAGAGGCGCGGATTTCTTTCTATACAGGCCAAGGTACAAAGCAAAATGCTTC 660  
Qy 221 TTYCysAspGluYGLuYLeuLYeAspTTPGluSerAspAspValProTTPGluGlnHisAla 240  
Db 661 TATTCGACGAGAGGCTTAAGAAAGATGGGAAAGCGATGACCTTCGTGGGAAACAGCAGCC 720  
Qy 241 ArgTTPPheAspArgCysAlaATyrValGlnLeuValLYeGluYArgArgTTPYrIleGlnLYe 260  
Db 721 AGATGTGTGACGCGCGCGGTACGTGCATTTGTATAAGAGACGTACATTCATTCAGAAAG 780  
Qy 261 ValLYeSerGluYAlaThrAlaIleSerAlaSerGluGluGluGlnAlaAlaThrAspAsp 280  
Db 781 GTGAACCTGGAGGCCACTGCGATATCTGTCAGGAAAGAAACAGGCCCGCACCAATGAT 840  
Qy 281 SerThrLYeAsnValAlaGlnGluGluYLYeHisLYeAspAspSerLYeLYeCysLYe 300  
Db 841 TCGACTAAAGAACTCCCTCAAGAGGCGGAGAAACATTTGGATGACTTAAGAAATGTAA 900  
Qy 301 ILeCysTyrSerGluYArgGluValCysPheValProCysGluYHisValAlaCys 320  
Db 901 ATATGTTATTTCCAGAGAGCGTAACTGTGTCTTGTGCGCGGACCGTGGCGGTGC 960  
Qy 321 AlaLYeCysAlaLeuSerThrAspLYeCysPProMetCysArgArgThrPheThrAsnAla 340  
Db 961 GCCAAATGCGCGCTGTGACGAGCAAGTGTCCGATGTGTGCGCAGACGTTCAAGAAATGCC 1020  
Qy 341 ValArgLeuYrPheSer 346  
Db 1021 GTGCGGCTCACTTCTCG 1038  
RESULT 4  
LOCUS AF195528 2614 bp mRNA linear INV 26-DEC-1999  
DEFINITION Trichoplistia n1 inhibitor of apoptosis protein (IAP1) mRNA,  
complete cds.  
ACCESSION AF195528  
VERSION AF195528.1 GI:6635436  
KEYWORDS Trichoplistia n1 (cabbage looper)  
SOURCE Trichoplistia n1  
ORGANISM Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
Neoptera; Endopterygota; Lepidoptera; Glossata; Dictyoptera;  
Noctuidae; Noctuidae; Plusiinae; Trichoplistia.  
REFERENCE 1 (bases 1 to 2614)  
Seshagiri,S., Vucic,D., Lee,J. and Dixit,V.M.

TITLE Baculovirus-based genetic screen for antiapoptotic genes identifies  
a novel IAP  
JOURNAL J. Biol. Chem. 274 (51), 36769-36773 (1999)  
PUBMED 10593985  
REFERENCE 2 (bases 1 to 2614)  
AUTHORS Seshagiri,S., Vucic,D., Lee,J. and Dixit,V.M.  
TITLE Direct Submission  
JOURNAL Submitted (15-OCT-1999) Molecular Oncology, Genentech Inc., 1 DNA  
Way, San Francisco, CA 94080, USA  
FEATURES  
source  
1. 2614  
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ORIGIN  
Alignment Scores:  
Pred. No.: 3.05e-86 Length: 2614  
Score: 1327.00 Matches: 251  
Percent Similarity: 79.67% Conservative: 39  
Best Local Similarity: 68.96% Mismatches: 54  
Query Match: 70.32% Indels: 20  
DB: 2 Gaps: 8  
US-10-041-859a-2 (1-346) x AF195528 (1-2614)  
Qy 1 MetGluLeuThrLYeValAlaLYeAsnGluYAlaAlaAlaThrLeuValMetLeuLYeAsn 20  
Db 174 ATGATATATAACCAAGTGGCATTCATGAGCCCGCTCACATTAACTTTTCAAGAAC 233  
Qy 21 Ala--ArgAspAlaLYeMetArgProPheIleGluYProLeuMetLeu-----SerSer 37  
Db 234 GCTCCGCGGAGCGCTAAGATTGACCTTATG--CCGCTAGTGTGGCGACGACGAGAC 290  
Qy 38 CysGluSerSerThrTherThrLeuProSerProSerSer----- 51  
Db 291 TACGACTCAAACGCGCGCTCTCCGGCTTGTCACCTCCACACCCCTCATCGTCTTTCTTCA 350  
Qy 52 ---SerAlaAspLYeThrAspAsnHisAspThrPheAsnPheLeuProAspMetProAsp 70  
Db 351 TTCTCATTTGACAAAGACGATTAACACGACACCTTAGTCTACCGCGGACCGGTGAT 410  
Qy 71 MetArgArgGluGluGluYArgLeuLYeThrPheAspGINTTPProValThrPheLeuThr 90  
Db 411 ATGAGCCGTGAAGACGACAAAGAAATTAACTTTTGAAATGCGCTGTCTCTTTATCC 470  
Qy 91 ProGluGluLeuAlaArgAnGIyPheYrTYrLeuGluYArgGluYAspGluValCysCys 110  
Db 471 GGGAGCAACTCGCCGAAACGAGATTTCTATACCTTTGGCGGAGATAGCTCCGATGC 530  
Qy 111 AlaPheCysLYeValGluIleMetArgTTPValGluGluYAspAspProAlaAlaAspHis 130  
Db 531 GCTTTTGAAGTGAATCATGAGATGGTTGAGGCGTGAAGACCCACCAAGATTCAC 590  
Qy 131 ArgArgTTPAlaProGlnCysProPheValArgLYeGImeTyrAlaAsnAlaGluYGLu 150  
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Db 591 CAGAGATGGGCGCCCAATGTCCTTTGTGAGGAAA---CTGGCGGCGGCTGTCAACACA 647  
Qy 151 GluAlaThrAlaValAlaGlyArgAspGluCyGlyValAspSerAlaIle-----ThrGlnPro 168  
Db 648 GACTCCGAGACTGCGCGCCGCGAGAGTGGCGCGGAGCTGCAACCACTCTCGCCC 707  
Qy 169 ProArgMetProGlyProValIleAlaArgTyrSerThrGluAlaAlaArgGluAlaThr 188  
Db 708 TCTCGCATGCTGGCGCTGTTCACCCCGCTATGCTCTGAAGCGCGCGCTGCGCAGT 767  
Qy 189 PheIleAspThrProAlaGlyMetArgGlnIlePheProGluIleGluAlaGlyPhe 208  
Db 768 TTTAAAGACTGGCCACATGCAATGCGACAAAGCGGAGAGCTGTGAGGCTGAGATTC 827  
Qy 209 PheTyrThrGlyGlnGlyAspIlePheThrLeuPhePheTyrCyAspArgGlyIleLeuIleAsp 228  
Db 828 TTTTACACTGTCGAGCGCGATTAAGACAAATGCTTTATTTGTATGATGCTGAGAGAT 887  
Qy 229 TrpGluSerAspAspValProTyrGluGlnIleAlaArgTyrPheAspArgCyAspIleTyr 248  
Db 888 TGGGAAAACAGACGCGCGCTGGAGCAACGCGCGGTGTTGACCGCTGCGCTTAC 947  
Qy 249 ValGlnIleValIleGlyArgAspTyrIleGlnIleValIlePheSerGluAlaThrAlaIle 268  
Db 948 GTCCAACTCGTGAAGAGACAGAAATACGTTCAAAAATGATGACAGAGCTTGCGTCAAT 1007  
Qy 269 -----SerAlaSerGluGluIle-----GlnAlaAlaThrAspSerThr 282  
Db 1008 CTGCACCGGACGCGCGACGAGCGCGCTGCGGCTCGCGCGCGGAGCCGAGCGT 1067  
Qy 283 LysAsnValAlaGlnGluGluIleLeuAspSerIleCyAspIleCyS 302  
Db 1068 GTCTCGCGCGTACGCGCGGAGAGATCTTAGACATTCAAAACGTCGCAAAATGCT 1127  
Qy 303 TyrSerGluIleValArgAsnValCyAspIleProCyGlyIleValIleAlaIleValIle 322  
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Qy 323 CysAlaIleSerThrAspIleValPheProMetCysArgArgThrPheThrAsnAlaValArg 342  
Db 1188 TGGCGCTGGACGCGCAAGTCCGATGTGCGCGGAGACGTTTCAGAAATGACGTGCG 1247  
Qy 343 LeuTyrPheSer 346  
Db 1248 TTATATTTCTCG 1259

RESULT 5  
AR340175 1134 bp DNA linear PAT 17-AUG-2003  
LOCUS AR340175  
DEFINITION Sequence 2 from patent US 6570069.  
ACCESSION AR340175  
VERSION AR340175.1 GI:33731574  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 1134)  
AUTHORS Hamcock,B.D., Huang,Q. and Maeda,S.  
TITLES Nucleic acids encoding plant inhibitors of apoptosis and transgenic  
cells and plants expressing them  
JOURNAL Patent: US 6570069-A 2 27-MAY-2003;  
Regents of the University of California; Oakland, CA  
FEATURES  
source  
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ORIGIN  
Alignment Scores:  
Pred. No.: 1.65e-85 Length: 1134  
Score: 1311.00 Matches: 248  
Percent Similarity: 79.28% Conservative: 39  
Best Local Similarity: 68.51% Mismatches: 57

Query Match: 69.48% Indels: 18  
DB: 6 Gaps: 7  
US-10-041-859a-2 (1-346) x AR340175 (1-1134)  
Qy 1 MetGluIleuThrIleValAlaIleValAsnGlyValAlaAlaThrIleuValMetLeuIleValAsn 20  
Db 52 ATGAGATATTTCAGAAAGGCGATCCAAATGGCTCTCTCCATCAATTAACGCTATTTCAGAGC 111  
Qy 21 ---AlaArgAspAlaIleValMetArgProPheIleGlyProIleuMetIleu-----SerSer 37  
Db 112 GGAATCGTTGAGCTTAAATTCACCT--CTGCGCCACTAAATGCTGCCAGCCCAAGT 168  
Qy 38 CysGluSerSerThrThrLeuProSerProSerSer----- 51  
Db 169 TAGAGCTCCAAACCCGCGCTCCATCTTTGCTCCATCCACGCGCTGCTTCATCTTCT 228  
Qy 52 ---SerAlaAspIleThrAspAsnIleAspThrPheAsnIleuProAspMetProAsp 70  
Db 229 TTTCTCCATTGATTAACCCGACCAACAGACACCTTGCGCTTCACTGCGGACAGATTGAT 288  
Qy 71 MetArgArgGluIleGluIleValGlyMetArgTyrValGluIleAspAspProAlaIleAspIle 90  
Db 289 ATGAGAAAAGAGATGAACGTATGAAAACATTTGAAAATGCGCCGTTAAGTTTCTATCC 348  
Qy 91 ProGluIleuAlaIleArgAsnGlyPheTyrTyrIleuGlyArgGlyAspGluValCyS 110  
Db 349 GAGAGACACTTCTCGTAATGATTTTACTACTGCGCGCTAGAGATGAAGCCGTTGC 408  
Qy 111 AlaPheCysIleValAlaGluIleMetArgTyrValGluIleAspAspProAlaIleAspIle 130  
Db 409 GCTTTCTGTAAGTGAAGATTAAGAGTGGAGGCGCATGACCTCGGAGAGACAT 468  
Qy 131 ArgArgTyrAlaIleProGlnIleCyAspIleValIleGlyMetIleValAlaAlaIleGlyIle 150  
Db 469 CACCGTTGGCGGCAACAGTCCCATTTGCGCAAA--TTGAACGCTACTGACAGCA 525  
Qy 151 GluAlaThrAlaValAlaGlyArgAspGluCyGlyValAspSerAlaIle-----ThrGln 167  
Db 526 GACACGGGTATGTCGCGCCAGAGAGATGTGTGCGCGCGCTCTCTCGGTACTCT 585  
Qy 168 ProProArgMetProGlyProValIleAlaArgTyrSerThrGluAlaAlaArgGluAla 187  
Db 586 CCGCGCGTATGGCGCGTCCGTGCAACCAATATGATCTGAAGCCGACCACTACGCG 645  
Qy 188 ThrPheIleAspThrProAlaGlyMetArgGlnIlePheProGluIleuAlaGlyIle 207  
Db 646 AGTTTAAAGACTGGCCACATGCAATGCGCAAAAACCTGMAAATCTCGCGAGGCTGCG 705  
Qy 208 PhePheTyrThrGlyGlnGlyAspIleValPheThrLeuPheTyrCyAspArgGlyIleuIle 227  
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Qy 228 AspTrpGluSerAspAspValProTyrGluGlnIleAlaArgTyrPheAspArgCyAspAla 247  
Db 766 GATTGGAGAAACATATGATGATCCCTGGGAACAAACAGAAAGTGTTGACCGTTGCGCC 825  
Qy 248 TyrValGlnIleuValIleGlyArgAspTyrIleGlnIleValIlePheSerGluAlaThrAla 267  
Db 826 TACGTGCAATTTGGTGAAGGCTCGAAGAAATCGTTCAAAAGCTGATTTCTGAAGCTTGAG 885  
Qy 268 IleSerAlaSerGluIleGluIle-----AlaAlaThrAsnAspSerThrIleValAsn 284  
Db 886 GATTCGCGCTCAAGAGCGAAGCATGATAGACCCGCGAGAGACTGCGCGCAAGCCCG 945  
Qy 285 ValAlaGlnIleuIleGlyIleuValIleuAspAspSerIleCyAspIleCyS/TyrSer 304  
Db 946 CACAGACAGGCGCGCAGAAAACCTGATGATGATCAAAAGTGTGTAATAATCTGTATGCT 1005  
Qy 305 GluGluIleuArgAsnValCyAspIleProCyGlyIleValIleValIleValIleValIle 324  
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Pred. No.: 2,71e-85 Length: 1739  
 Score: 1311.00 Matches: 248  
 Percent Similarity: 79.28% Conservative: 39  
 Best Local Similarity: 68.51% Mismatches: 57  
 Query Match: 69.48% Indels: 18  
 DB: 6 Gaps: 7

US-10-041-859a-2 (1-346) x AR340174 (1-1739)

1 MetGluLeuThrLysValAlaLysAsnGlyAlaAlaThrLeuValMetLeuLysAsn 20  
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 21 --AAlaArgAspAlaLysMetArgProPheIleGlyProLeuMetLeu-----SerSer 37  
 340 GGATCGCTTGAAGCTAAATAATCGACCT--CTCGGCGCACTAATGCTGCGAGCCCAAGT 396  
 38 CysGluSerSerThrThrSerThrLeuProSerProSerSer----- 51  
 397 TACGACTCCAAAGCCGCGCTCTCCATCTTGTCTCCATCCACAGCCCTTGTCTTCATCTTCT 456  
 52 ---SerAlaAspLysThrAspAsnHisAspThrPheAsnPheLeuProAspMetProAsp 70  
 457 TTCTTCATTGATTAACCAACCAACCAACCACTTTCGCTTCAGTCCGACACAGTGTAT 516  
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 517 ATGAGAAAAGAGATGATACGTATGAAAACATTGAAAATGGCCCGCTAAGTTTCTTATCC 576  
 91 ProGluGlnLeuAlaArgAsnGlyPheTyrrTyrrLeuGlyArgGlyLysAspGluValCysCys 110  
 577 GGAGAGCAACTGCTCGAAATGATTTTACTCTGCGCGCTGAGAGATGAAGCCCTTGC 636  
 111 AlaPheCysLysValGluIleMetArgTrpValGluGlyAspAspProAlaAlaAspHis 130  
 637 GCTTCTGTAAGTGAAGATTAATGAGTGGGTGAGAGCGGATACCTCGGAAGGACCAT 696  
 131 ArgArgTrpAlaProGlnCysProPheValArgLysGlnMetTyrrAlaAsnAlaGlyGly 150  
 697 CAGCGTGGGGCGGCACAGTGCCATTGTGGCGCAA--TTGAACGGTACTGACAGCAGCA 753  
 151 GluAlaThrAlaValGlyArgAspGlyCysGlyAlaSerAlaAla-----ThrGln 167  
 754 GACACGGGATGTCGGGCGCAGAGAGTGTGGTGGCGCGCCCTCCCTCCGGTACTCTCT 813  
 168 ProProArgMetProGlyProValHisAlaArgTyrrSerThrGlnAlaAlaArgLeuAla 187  
 814 CCGCGCGGTAATGGCCGCTCCCTGTCACCCACGATATGATCTGAACCCGACAGACTACGC 873  
 188 ThrPheLysAspTrpProArgArgMetArgGlnLysProGluGluLeuAlaGluAlaGly 207  
 874 AGTTTAAAGACTGGCCAGATGATGATGCACAAAAACCTGAAGAACTCCGCCGAGCTGGC 933  
 208 PhePheTyrrThrGlyGlnGlyAspLysThrLysCysPheTyrrCysAspGlyGlyLeuLys 227  
 934 TTTTATTACACTGGTGAAGGAGCAAAACCAACTGTTTTATTGTCATGGTGAATTAATA 993  
 228 AspTrpGluSerAspAspValProTrpGluGlnHisAlaArgTrpPheAspArgCysAla 247  
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 LOCUS Sequence 1 from Patent WO0159108.  
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 ACCESSION AX213188  
 VERSION AX213188.1 GI:15524132  
 KEYWORDS  
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 Spodoptera frugiperda (fall armyworm)  
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 REFERENCE  
 1 Maeda,S.D., Huang,Q. and Maeda,H.E.  
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 Patent: WO 0159108-A 1 16-AUG-2001;  
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# ORIGIN

## Alignment Scores:

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 Score: 1311.00 Matches: 248  
 Percent Similarity: 79.28% Conservative: 39  
 Best Local Similarity: 68.51% Mismatches: 57  
 Query Match: 69.48% Indels: 18  
 DB: 6 Gaps: 7

US-10-041-859a-2 (1-346) x AX213188 (1-1739)

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QY	228	AspTrpGlnSerAspAspValProTrpGluGlnHisAlaArgTrpPheAspArgCysAla	247
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LOCUS	U53466	123500 bp	DNA
DEFINITION	Cydia pomonella granulovirus, complete genome.		circular VRL 14-NOV-2001
ACCESSION	U53466	AB010886	L05494 U48447 Y09478
VERSION	U53466.2	GI:14591762	
KEYWORDS	Cydia pomonella granulovirus		
SOURCE			

ORGANISM	REFERENCE	AUTHORS	TITLE
Cydia pomonella granulovirus	1 (bases 1 to 123500)	Crook,N.E., Clem,R.J., and Miller,L.K.	An apoptosis-inhibiting Baculovirus gene with a zinc finger-like motif
JOURNAL	J. Virol. 67 (4), 2168-2174 (1993)		
PUBMED	8445726		
REFERENCE	2 (bases 1 to 123500)	Theilmann,D.A., Chantlier,J.K., Stewart,S., Filipsen,H.T., Vlak,J.M. and Crook,N.E.	Characterization of a highly conserved baculovirus structural protein that is specific for occlusion-derived virions
TITLE	Virology 218 (1), 148-158 (1996)		
JOURNAL	8615018		
PUBMED	3 (bases 1 to 123500)	Kang,W., Crook,N.E., Winstanley,D. and O'Reilly,D.R.	Complete sequence and transposon mutagenesis of the BamHI J fragment of Cydia pomonella granulosis virus
REFERENCE	4 (bases 1 to 123500)	Kang,W., Tristram,M., Maeda,S., Crook,N.E. and O'Reilly,D.R.	Identification and characterization of the Cydia pomonella granulovirus cathepsin and chitinase genes
TITLE	J. Gen. Virol. 79 (Pt 9), 2283-2292 (1998)		
JOURNAL	9747739		
PUBMED	5 (bases 1 to 123500)	Lague,T., Finch,R., Crook,N., O'Reilly,D.R. and Winstanley,D.	The complete sequence of the Cydia pomonella granulovirus genome
REFERENCE	6 (bases 1 to 123500)	Crook,N.E.	
TITLE	Direct Submission		
JOURNAL	Submitted (11-JUN-1993)	Entomological Sciences, Horticulture Research International, Wellesbourne, Warwickshire CV35 9EF, UK	
PUBMED	7 (bases 1 to 123500)	Crook,N.E.	
REFERENCE	8 (bases 1 to 123500)	Kang,W., Crook,N.E., Winstanley,D. and O'Reilly,D.R.	Direct Submission
TITLE	Submitted (03-APR-1996)	Imperial College of Science, Technology and Medicine, Imperial College Road, SAF Building, 5th floor, London SW7 2AZ, UK	
JOURNAL	9 (bases 1 to 123500)	Crook,N.E., James,J.D., Smith,I.R.L. and Winstanley,D.	Direct Submission
PUBMED	10 (bases 1 to 123500)	Kang,W.	Submitted (15-NOV-1996)
REFERENCE	11 (bases 1 to 123500)	Entomological Sciences, Horticulture Research International, Wellesbourne, Warwickshire CV35 9EF, UK	
TITLE	Submitted (03-FEB-1998)	Lab. of Mol. Entomol. and Baculovirology, RIKEN, 2-1 Hiroxawa, Wako, Saitama 351-0198, Japan	
JOURNAL	12 (bases 1 to 123500)	Lague,T., Finch,R., Crook,N., O'Reilly,D.R. and Winstanley,D.	Direct Submission
PUBMED	13 (bases 1 to 123500)	Imperial College of Science, Technology and Medicine, Imperial College Road, SAF Building, 5th floor, London SW7 2AZ, UK	
REFERENCE	14 (bases 1 to 123500)	Sequence update by submitter	
TITLE	On or before Jun 3, 2001 this sequence version replaced gi:3273310.		
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TITLE	Location/Qualifiers		
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TITLE	Location/Qualifiers		
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PUBMED	25 (bases 1 to 123500)	Location/Qualifiers	
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TITLE	Location/Qualifiers		
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REFERENCE	29 (bases 1 to 123500)	Location/Qualifiers	
TITLE	Location/Qualifiers		
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TITLE	Location/Qualifiers		
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REFERENCE	44 (bases 1 to 123500)	Location/Qualifiers	
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TITLE	Location/Qualifiers		
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PUBMED	49 (bases 1 to 123500)	Location/Qualifiers	
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TITLE	Location/Qualifiers		
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PUBMED	52 (bases 1 to 123500)	Location/Qualifiers	
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Qy	168	-----ProPArgMetProGlyProValHisAlaArgTyrSer	180
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Dp	13185	CATGAAGCTGTGTCAGTCACAGAGTTTTCACAACTGGCCCCGTTGTATGAAGACAGACCC	13244
Qy	201	GluGluLeuAlaGlyAlaGlyPhePheTyrThrGlyGlnGlyAspTyrThrTyrCysPhe	220
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DEFINITION	Anticarsia gemmatilis nucleopolyhedrovirus IAP-3 gene, complete cds.		
ACCESSION	AY525121		
VERSION	AY525121.1	GI:46401441	
KEYWORDS	Anticarsia gemmatilis nucleopolyhedrovirus		
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ORGANISM	Virus; dsDNA viruses, no RNA stage; Baculoviridae; Nucleopolyhedrovirus.		
REFERENCE	1 (bases 1 to 1247)		
AUTHORS	Carper,M.P., Castro,M.E., Soares,E.F., Villela,A.G., Pinedo,F.J. and Ribeiro,B.M.		
TITLE	Characterization of the inhibitor of apoptosis gene (Iap-3) gene of Anticarsia gemmatilis multicapsid nucleopolyhedrovirus (AgMPV)		
JOURNAL	Unpublished		
REFERENCE	2 (bases 1 to 1247)		
AUTHORS	Carper,M.P., Castro,M.E., Soares,E.F., Villela,A.G., Pinedo,F.J. and Ribeiro,B.M.		
TITLE	Direct Submission		
JOURNAL	Submitted (13-JAN-2004) Cell Biology, University of Brasilia, Campus Universitario Darcy Ribeiro UnB, Brasilia, DF 70910-900, Brazil		
FEATURES	Location/Qualifiers		
SOURCE	1..1247		

CDs

US-10-041-859A-2 (1-346) x AY525121 (1-1247)

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Db	937	AAATATCTGTGACGACAAATTAAACAGGTTCGACAAACCCGCAAAATCAATTACCAAA	996	REMARK	Sequence update by submitter
Db	937	AAATATCTGTGACGACAAATTAAACAGGTTCGACAAACCCGCAAAATCAATTACCAAA	996	COMMENT	On Jan 21, 2005 this sequence version replaced gi:37499238.
Oy	296	SeelysileCyblysileCyetyserglugluAgaanvalCyephvalProCyagly	315	FEATURES	Location/Qualifiers
Db	997	AACAAATGTCMAATTTGCTTGGCTGTGAAAACAGTGTGTTGATCCGCGGT	1056	source	1. .131160
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Db	1057	CACGTGTGGGTGGCGCAATGCCCAATTGTATTAAGATTGCCCATGTGCCGCGCA	1116		nucleopolyhedrovirus"
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RESULT 12					join(129351..131160,1..20)
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REFERENCE	1 (bases 11500 to 13512)				VLASIVARIENILSDAVNDVEITVLSGDFEESRSRATROYVSTDLTLPPLPLPLP
AUTHORS	Barrett,J.W., Krell,P.J. and Arif,B.M.				PETTOAFVAPSPPAQAFVAPSPPAQAFVAPSPPAQAFVAPSPPAQAFVAPSPPAQ
TITLE	Characterization, sequencing and phylogeny of the ecdyseroid UDP-glucosyltransferase gene from two distinct nuclear polyhedrosis viruses isolated from Choristoneura fumiferana				FVAPSPPAQAFVAPSPPAQAFVAPSPPAQAFVAPSPPAQAFVAPSPPAQAFVAP
JOURNAL	J. Gen. Virol. 76 (Pt 10), 2447-2456 (1995)				NGVNLNTLTKPPVPPKPAHLSRPVFMVGDVKTGNTPTPNGTSPROGAVVPPVAP
REFERENCE	2 (bases 13243 to 14241)				PLNWPPPPPPVPPPPPLDNLIDAMMSERKANTDRSALFDQIKMGTAKKQVPE
AUTHORS	Barrett,J.W., Lauzon,H.A., Mercuri,P.S., Krell,P.J., SohI,S.S. and Arif,B.M.				PPSRLRGDMLNQIRGATLRTGRLEDENLGPKRGRLIGVLTNTLGSRRGIDS
TITLE	The putative DEF-1 proteins from two distinct Choristoneura fumiferana multiple nucleopolyhedroviruses share domain homology to eukaryotic primases				RSDVATSESTSGPDESADTRADKASKSELKHAHLVYNKAKSKLYNIQKVNSELTKI
JOURNAL	Virus Genes 13 (3), 229-237 (1996)				LENVGPLKRSRPTAENYEKANAGLYLFRQHTLIPKNALDQAPAPELVADAPQFYVO
REFERENCE	3 (bases 80268 to 81693)				IEDLIFAGRVDADFIQVADAPEDMKLKKFLVIANQLSTRGQ"
AUTHORS	Li,X., Lauzon,H.A., Sohl,S.S., Palli,S.R., Retnakaran,A. and Arif,B.M.				complement(1..738)
TITLE	Molecular analysis of the p48 gene of Choristoneura fumiferana multicapsid nucleopolyhedroviruses CFMNPV and CFDEFNPV				/note="ORF 1; ph Op3/Ac8, major occlusion body protein"
JOURNAL	J. Gen. Virol. 80 (Pt 7), 1833-1840 (1999)				/codon start=1
REFERENCE	4 (bases 1 to 131160)				/product="polyhedrin"
AUTHORS	Li,X., Barrett,J., Pang,A., Klose,R.J., Krell,P.J. and Arif,B.M.				/protein_id="AA091696.1"
TITLE	Characterization of an overexpressed spindle protein during a baculovirus infection				/db_xref="GI:37499297"
JOURNAL	Virolgy 268 (1), 56-67 (2000)				/translation="MPNYSVPPTGRVYVYNNKYKNGSVIKNAKKKHLLHEBDE
REFERENCE	5 (bases 1 to 131160)				KHLDPLDHYMAEDPFLGPGKKQKTLTEKEIRANKEPDMKLIYVMSGSEPLREMTFR
AUTHORS	Lauzon,H.A., Jamieson,P.B., Krell,P.J. and Arif,B.M.				VEDSPPIVNDQVMDVFLVILNRPTRPCRYKFLQHLRMDCDVPEHVRIRIVPSY
TITLE	Gene organization and sequencing of the Choristoneura fumiferana defective nucleopolyhedrovirus genome				VGMNNEYRISLAKGSGCPIMNISEYNSFESFVNRVIMENFYIYIGTDSGEE
JOURNAL	J. Gen. Virol. 86 (Pt 4), 945-961 (2005)				ELIEVSLVFKKEFAPADPAFLPTGPAY"
REFERENCE	15784888				complement(828..1220)
AUTHORS	Lauzon,H.A., Jamieson,P.B., Krell,P.J. and Arif,B.M.				/note="ORF 2; Op5"
TITLE	Submitted (20-JUN-2003) Molecular Virology, Great Lakes Forestry Centre, 1219 Queen St. E., Sault Ste. Marie, Ontario P6A 2B5, Canada				/codon start=1
JOURNAL	7 (bases 1 to 131160)				/product="unknown"
REFERENCE	Lauzon,H.A.M., Jamieson,P.B., Krell,P.J. and Arif,B.M.				/protein_id="AA091742.1"
AUTHORS	Submitted (21-JAN-2005) Molecular Virology, Great Lakes Forestry Centre, 1219 Queen St. E., Sault Ste. Marie, Ontario P6A 2B5, Canada				/db_xref="GI:37499343"
JOURNAL	Submitted (21-JAN-2005) Molecular Virology, Great Lakes Forestry Centre, 1219 Queen St. E., Sault Ste. Marie, Ontario P6A 2B5, Canada				/translation="MADSTNRTRLRFYRWSSKTSGLSENQADLECTYLDERFVGAHMN
REFERENCE	9035367				KOITSCKKKKQAEERASALKRYELADRAAKAPYACADGGRRSTLSQOLED
AUTHORS	Li,X., Lauzon,H.A., Sohl,S.S., Palli,S.R., Retnakaran,A. and Arif,B.M.				IDRKEIVDRILYKQLKQDCCLNNNAF"
TITLE	Molecular analysis of the p48 gene of Choristoneura fumiferana multicapsid nucleopolyhedroviruses CFMNPV and CFDEFNPV				complement(1247..1858)
JOURNAL	J. Gen. Virol. 80 (Pt 7), 1833-1840 (1999)				/note="ORF 3; 1ef-2 Op6/Ac6"
REFERENCE	10423153				/codon start=1
AUTHORS	Li,X., Barrett,J., Pang,A., Klose,R.J., Krell,P.J. and Arif,B.M.				/product="late expression factor 2"
TITLE	Characterization of an overexpressed spindle protein during a baculovirus infection				/protein_id="AA091716.1"
JOURNAL	Virolgy 268 (1), 56-67 (2000)				/db_xref="GI:37499317"
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AUTHORS	Lauzon,H.A., Jamieson,P.B., Krell,P.J. and Arif,B.M.				FEMSGRLRALITAPKPTPEKAVILHSKRVNCLKACDGSVNLAKALNLSRMLPCM
TITLE	Gene organization and sequencing of the Choristoneura fumiferana defective nucleopolyhedrovirus genome				VKIMEILNNAASPRGMYRKREFTCYGNVVSCTKCSACLICGLHLHRYKMDPRCVG
JOURNAL	J. Gen. Virol. 86 (Pt 4), 945-961 (2005)				EVTHLLIKAEDEVYKRCNAKMKTKVNLCPKAMCKGKPIGNF"
REFERENCE	15784888				complement(1861..2124)
AUTHORS	Lauzon,H.A., Jamieson,P.B., Krell,P.J. and Arif,B.M.				/note="ORF 4; Op7/Ac5"
TITLE	Submitted (20-JUN-2003) Molecular Virology, Great Lakes Forestry Centre, 1219 Queen St. E., Sault Ste. Marie, Ontario P6A 2B5, Canada				/codon start=1
JOURNAL	6 (bases 1 to 131160)				/product="unknown"
REFERENCE	Lauzon,H.A.M., Jamieson,P.B., Krell,P.J. and Arif,B.M.				/protein_id="AA091760.1"
AUTHORS	Submitted (21-JAN-2005) Molecular Virology, Great Lakes Forestry Centre, 1219 Queen St. E., Sault Ste. Marie, Ontario P6A 2B5, Canada				/db_xref="GI:37499361"
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REFERENCE	2171..2608				TGFDNCRILIELSSSNDVITKSPVITIKSAAATVGSGALVCXY"
AUTHORS	Lauzon,H.A.M., Jamieson,P.B., Krell,P.J. and Arif,B.M.				/note="ORF 5; Op8/Ac4"
TITLE	Submitted (21-JAN-2005) Molecular Virology, Great Lakes Forestry Centre, 1219 Queen St. E., Sault Ste. Marie, Ontario P6A 2B5, Canada				/codon start=1
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REFERENCE	Lauzon,H.A.M., Jamieson,P.B., Krell,P.J. and Arif,B.M.				/protein_id="AA091737.1"
AUTHORS	Submitted (21-JAN-2005) Molecular Virology, Great Lakes Forestry Centre, 1219 Queen St. E., Sault Ste. Marie, Ontario P6A 2B5, Canada				/db_xref="GI:37499338"
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REFERENCE	2647..3657				HBEGFLDRNALVACMAVNVQVYDPDGITRLNPKTIYFVCCQKCHAVADVAPADHDSI
AUTHORS	Lauzon,H.A.M., Jamieson,P.B., Krell,P.J. and Arif,B.M.				ARYLCAACGMVLIQHPDVFQDTEBGVVELLEVORINAGDL"
TITLE	Submitted (21-JAN-2005) Molecular Virology, Great Lakes Forestry Centre, 1219 Queen St. E., Sault Ste. Marie, Ontario P6A 2B5, Canada				
JOURNAL	Submitted (21-JAN-2005) Molecular Virology, Great Lakes Forestry Centre, 1219 Queen St. E., Sault Ste. Marie, Ontario P6A 2B5, Canada				

Alignment Scores:

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Percent Similarity:	69.26%	Conservative:	35
Best Local Similarity:	56.89%	Mismatches:	76
Query Match:	47.19%	Indels:	11
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QY 88 PheLeuThrProGluGlnLeuAlaArgAsnGlyPheTYrTrpLeuGluValArgGlyAspGlu 107	QY 128 AlaAspHisArgArgTrpAlaProGlnCysProPheValArgLys-----GlnMet 144
Db 24046 TTTTGTGAACCAAGTCAAAATGGCCGCCCAACGGGTTTATCTATTGAGGCGCTCGACGAG 23987	Db 23926 GTAGATCATTAACGATGGGACCGGACGCGCTCCGTTGTGTGCACAGAAATCTGCACACAG 23867
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DEFINITION	Choristoneura fumiferana MNV polyhedrin, complete genome.				

ACCESSION	AF512031	AF177329	S46001	S78506	S81690	U10441	U18677	U26676	U26734
VERSION	US3854	US7401	US9008	U70432	U72240	X65395			
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REFERENCE	1	(bases 1 to 129593)							
AUTHORS	Lee, H.Y., Arif, B., Dobos, P. and Krell, P.								
TITLE	Identification of bent DNA and ARS fragments in the genome of Choristoneura fumiferana nuclear polyhedrosis virus								
JOURNAL	Virus Res.	24	(3),	249-264	(1992)				
PUBMED	1413988								
REFERENCE	2	(bases 1 to 129593)							
AUTHORS	Xie, W.D., Arif, B., Dobos, P. and Krell, P.J.								
TITLE	Identification and analysis of a putative origin of DNA replication in the Choristoneura fumiferana multinucleocapsid nuclear polyhedrosis virus genome								
JOURNAL	Virology	209	(2),	409-419	(1995)				
PUBMED	7778276								
REFERENCE	3	(bases 1 to 129593)							
AUTHORS	Liu, J.J. and Carstens, E.B.								
TITLE	Identification, localization, transcription, and sequence analysis of the Choristoneura fumiferana nuclear polyhedrosis virus DNA polymerase gene								
JOURNAL	Virology	209	(2),	538-549	(1995)				
PUBMED	7778286								
REFERENCE	4	(bases 1 to 129593)							
AUTHORS	Barrett, J.W., Krell, P.J. and Arif, B.M.								
TITLE	Characterization, sequencing and phylogeny of the ecdyseroid UDP-glucosyltransferase gene from two distinct nuclear polyhedrosis viruses isolated from Choristoneura fumiferana								
JOURNAL	J. Gen. Virol.	76	(Pt 10),	2447-2456	(1995)				
PUBMED	7595348								
REFERENCE	5	(bases 1 to 129593)							
AUTHORS	Qiu, W., Liu, J.J. and Carstens, E.B.								
TITLE	Studies of Choristoneura fumiferana nuclear polyhedrosis virus gene expression in insect cells								
JOURNAL	Virology	217	(2),	564-572	(1996)				
PUBMED	8610448								
REFERENCE	6	(bases 1 to 129593)							
AUTHORS	Liu, J.J. and Carstens, E.B.								
TITLE	Identification, molecular cloning, and transcription analysis of the Choristoneura fumiferana nuclear polyhedrosis virus spindle-like protein gene								
JOURNAL	Virology	223	(2),	396-400	(1996)				
PUBMED	8806578								
REFERENCE	7	(bases 1 to 129593)							
AUTHORS	Lapointe, R., Back, D.W., Ding, Q. and Carstens, E.B.								
TITLE	Identification and molecular characterization of the Choristoneura fumiferana multinucleocapsid nucleopolyhedrovirus genomic region encoding the regulatory genes pkip, p47, lef-12, and gta								
JOURNAL	Virology	271	(1),	109-121	(2000)				
PUBMED	10814576								
REFERENCE	8	(bases 1 to 129593)							
AUTHORS	Carstens, E.B., Liu, J.J. and Dominy, C.								
TITLE	Identification and molecular characterization of the baculovirus CfMNPV early genes: le-1, le-2 and p638								
JOURNAL	Virus Res.	83	(1-2),	13-30	(2002)				
PUBMED	11864738								
REFERENCE	9	(bases 1 to 129593)							
AUTHORS	de Jong, J.G., Lauzon, H.A., Dominy, C., Polowinski, A., Carstens, E.B., Arif, B.M. and Krell, P.J.								
TITLE	Analysis of the Choristoneura fumiferana nucleopolyhedrovirus genome								
JOURNAL	J. Gen. Virol.	86	(Pt 4),	929-943	(2005)				
PUBMED	15784887								
REFERENCE	10	(bases 1 to 129593)							
AUTHORS	de Jong, J.G., Dominy, C.N., Lauzon, H.A., Arif, B.M., Carstens, E.B. and Krell, P.J.								
TITLE	Direct Submission								
JOURNAL	Submitted (13-MAY-2002)								

REFERENCE	11	(bases 1 to 129593)	Guelph, Chemistry and Microbiology Building, Guelph, ON N1G 2W1, Canada
AUTHORS	de Jong, J.G., Dominy, C.N., Lauzon, H.A., Arif, B.M., Carstens, E.B. and Krell, P.J.		
TITLE	Direct Submission		
JOURNAL	Submitted (13-MAY-2004)	Department of Microbiology, University of Guelph, Chemistry and Microbiology Building, Guelph, ON N1G 2W1, Canada	
REMARK	Sequence update by submitter		
REFERENCE	12	(bases 1 to 129593)	de Jong, J.G., Dominy, C.N., Lauzon, H.A., Arif, B.M., Carstens, E.B. and Krell, P.J.
AUTHORS	Direct Submission		
TITLE	Submitted (19-JAN-2005)	Department of Microbiology, University of Guelph, Chemistry and Microbiology Building, Guelph, ON N1G 2W1, Canada	
JOURNAL	Sequence update by submitter		
REMARK	On Jan 19, 2005 this sequence version replaced gi:47157118.		
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cds.  
ACCESSION AB088850  
VERSION AB088850.1 GI:27923007  
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SOURCE Hyphancrtria cunea nucleopolyhedrovirus  
ORGANISM Hyphancrtria cunea nucleopolyhedrovirus  
Viruses; dedNA viruses, no RNA stage; Baculoviridae;

**Nucleopolyhedrovirus.**

REFERENCE  
1  
Ikeda, M., Yanagimoto, K. and Kobayashi, M.

**TITLE** Identification and functional analysis of nymphaeilla cutes nucleopolyhedrovirus iap genes  
**JOURNAL** Virology 321 (2), 359-371 (2004)  
**ISSN** 0022-2675

REFERENCE 2 (bases 1 to 1241)

**AUTHORS** Ikeda, M. and Kobayashi, M.  
**TITLE** Direct Submission  
**JOURNAL** Submitted (26-JUL-2002) Motoko Ikeda, Nagoya University, Graduate School of Science, Department of Chemistry, Gokisocho-1, Chikusa-ku, Nagoya 464-8602, Japan  
**ABSTRACT** The direct submission of a manuscript to the Journal is possible. The author should submit the manuscript to the Journal directly, without going through the editorial board. The author should submit the manuscript to the Journal directly, without going through the editorial board. The author should submit the manuscript to the Journal directly, without going through the editorial board.

## FEATURES

### Location/Qualifiers

US-10-041-859A-2 (1-346) X AB088850 (1-1241)

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QY	150	GlyGluAlaThrValaGlyArgAspGluCysGlyAlaSerAlaAlaThrGlnProPro	169
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[illegible]

RESULT	15
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LOCUS	CFU82510
DEFINITION	Choristoneura fumiferana nucleopolyhedrovirus apoptosis inhibitor
ACCESSION	U62510
VERSION	U62510.1 GI:4099075

SOURCE	Choristoneura fumiferana NMV
ORGANISM	Choristoneura fumiferana NMV viruses; no RNA stage; Baculoviridae; Nucleopolyhedrovirus.
REFERENCE	1 (bases 1 to 1032)
AUTHORS	Lauzon,H., Atif,B.M., Ladd,T. and Palli,R.
TITLE	CfNMV IAP gene

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FEATURES
source      location/Qualifiers
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ORIGIN

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US-10-041-859A-2 (1-346) x CF082510 (1-1032)

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